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ALIGNMENTS

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Adz13518 F
Adc52548 F
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Abg31740 F
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Abg13501 F
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ADZ13510 ADZ13516 ADZ13508 AAE02358 AAE023548 AAB31740 ABB31740 ABB31740 ADZ13503 AAE05518 AAB843195 AAB843195 AAB843195 AAB843195 AAB843195 AAB843195 AAB843195

2211.5 2211.5 2200.6 2200.6 2200.6 2200.6 200.7

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Aae20962 Human TR2
Adi21099 Novel hum
Aab88406 Human mem
Ady63175 Human Clo
Aam23972 Human Clo
Adi21579 Novel hum
Abb50346 Human sec
Abb50346 Human pro
Abb50685 Human pro
Aae20965 Human Rec
Abb50685 Human Rec
                                                        February 23, 2006, 12:00:35; Search time 187 Seconds (without alignments) 636.747 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                      1 MAPRALPGSAVLAAAVFVGG......ETVNGEVPATPVKRERSGTE
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Adb8406
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Abb50346
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Abb50685
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Adb2042
Abb20655
Adb2042
GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                            2443163 seqs, 439378781 residues
                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                        OM protein - protein search, using sw model
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AAM23972
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Gapop 10.0 , Gapext 0.5
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geneseqp2000s: *
geneseqp2002s: *
geneseqp2003as: *
geneseqp2003as: *
geneseqp2003bs: *
geneseqp2004s: *
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geneseqp1980s:*
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Maximum DB seq length: 200000000
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No.
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				immune disorder;	ison's disease;	ir disorder; epilepsy; disease; infection;	antiproliferative;	antibacterial;		-	-				-						-					-					
; 271 AA.	_			Human; tumour necrosis factor receptor; TNF; TR21; TR22; immune disorder;	nia; rheumatoid arthritis; Addison's disease;	allergy; cancer; ulcerative colitis; cardiovascular disorder; epilepsy myocardial ischaemia; wound healing; neurological disease; infection;	cerebral anoxia; gene therapy; immunosuppressive; antipr	cytostatic; cardiant; vasotropic; neuroprotective; antib virucide; fungicide; nootropic; ophthalmological.			alifiers		Signal_peptide	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	.taber= 1000000000000000000000000000000000000	/label= Mature_TR21_protein	:	Label= Immunogenic_epitope 09116	label= Immunogenic_epitope	1	label= Immunogenic_epitope 68. 173	label= Immunogenic_epitope	.92199 346 - Immineconfo ordinare	uniogenic_epicope	label= Immunogenic_epitope	133238 Jahola Tmminosonis enitone		label= Immunogenic_epitope			
T 1 962 AAE20962 standard, protein, 271		(first entry)	Human TR21 receptor protein	r necrosis fact	autoimmune haemolytic anaemia;	ser; ulcerative schaemia; wound	cia; gene thera	cardiant, vasot gicide, nootro			Location/Onalifiers	129		2956	30271	/label= Mat	8187	/label= Imm 109116	/label= Imm	142149	/label= Imm 168173	/label= Imm	192199	204218	/label= Imm	233238 /label= Imm	262271	/label= Imm	11.		
RESULT 1 AAE20962 ID AAE20962 Btam	AAE20962;	01-JUL-2002	Human TR21 re	Human; tumou	autoimmune ha	allergy; cand myocardial is	cerebral ano	cytostatic; c		Homo sapiens	Kev	Peptide		Region	Protein		Region	Region	,	Region	Region		Region	Region)	Region	Region		WO200207762-A1		31-JAN-2002.
RESI AAE ID	AC.	\$8\$	智	X.	Æ.	KW	KW	KW	×	S S	報	F	FF		T. E.	FT	됩		FT	FI		F	E E	1 E	FT		: E	LA	XX NA	X:	04 -

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AAE20965 ABO44942 ABO24423 ADP29451 ADP29451 AAY41111 AAY47078 AAE05517 AAG09901 ABG31739 ABG31739 ABG31739 ABG83983

Abg31739 B Ada83983 B Abo84934 B

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                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel human tumour necrosis factor (TNF) receptors, TR21 and TR22 and polynucleotides encoding them. Sequences of the invention are useful in the diagnosis, treatment and prevention of cancers (e.g., cancers of the adrenal gland, bone, urogenital or bone marrow, in particular breast and ovarian cancer), immune disorders (e.g., autoimmune haemolytic anaemia, rheumatoid arthritis, allergies, Addison's disease, ulcerative colitis), cardiovascular disorders (e.g., myocardial ischaemias), wound healing, neurological diseases (e.g., crebral anoxia, epilepsy) and infectious diseases such as viral, bacterial, fungal and sequence is human TR21 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; none cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue replacement; burn; incision; ulcer; cancer; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEBEEKVEKIELNDSVNENSDTVGQI 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                   Two novel proteins, TR21 and TR22, which are members of the tumor necrosis factor receptor, useful for the diagnosis and treatment of immune disorders, cancer, cardiovascular disorders.
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                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                             Ruben SM, Rosen CA;
                  23-JUL-2001; 2001WO-US023124
                                                    2000US-0220116P
2000US-0221143P
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N-PSDB; AAD33366.
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                                                24-JUL-2000;
                                                                      27-JUL-2000;
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The invention relates to an isolated polymucleotide encoding a polypeptide with biological activity. The polymucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polymucleotides may also be used as molecular weight markers, craise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in the sources of a corresponding received the antiple of burns and ulcers, and in treating cancer. The corresponding received the antiple of the antiple of
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                                                                                                                                                                                                                                                                                                                                                                Wang J;
Wang D;
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Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT,
Haley-Vicente D;
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Pred. No. 1.1e-120;
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100.0%; Pred. No. 1...
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                                                                                                                                                                                19-SEP-2002; 2002WO-US029964.
                                                                                                                                                                                                                                   19-SEP-2001; 2001US-0323739P
                                                                                                                                                                                                                                                         13-SEP-2002; 2002US-00323739
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N-PSDB; ADI21815.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 271 AA;
                                                                           WO2003025148-A2
                        Homo sapiens.
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                                                                                                                               27-MAR-2003
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RESULT

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121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPPGFPGGTPGKHVCGHHL
                                      VHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVCGHHL
                                                                                                                                          HTVGGVVERDVCHRCRHKRWHF1KPTNKSRESRPRRQGEVTVLSVGRPRVTKVEHKSNQK
                                                                                                                                                                                                                                               ERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-MAR-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADY63175;
                                      121
                                                                                                                                          181
                                                                                                                                                                                                                                               241
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                                                                                                                                                                                                                                                                                                                                                                                                  ADY63175

ID ADY6

XX ADY6

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XX BP15

XX Gene

XX BP15

XX BP15

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    which encode human secretory or membrane proteins represented by AARPS910 A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding secretory proteins/membrane proteins, useful gene therapy or as candidate target molecules in drug development.
                                                                                                                                                                                                                                       Human; secretory protein; membrane protein; vaccine; gene therapy;
rheumatoid arthritis; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 180; 609pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This invention relates to nucleic acid sequences AAF93744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isogai T, Nishikawa T, Kawai Y, Sugiyama T,
                                                                                                                                                                                        Human membrane or secretory protein clone PSEC0162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Prec. ....
                           AAB88406 standard; protein; 271 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99JP-00194179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUL-2000; 2000EP-00114090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAY-2000; 2000JP-00183766.
                                                                                                                                  (first entry)
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Matches 270; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAF93833
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                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                      EP1067182-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            08-JUL-1999;
11-JAN-2000;
                                                                                                                                  23-MAY-2001
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                                                                              AAB88406;
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AAB88406
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YALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEBEKVEKIELNDSVNENSDTVGQI 120

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel human secretory proteins or membrane proteins, and their coding sequences. The present sequence is one such protein sequence. The coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1421; DB 9;
Pred. No. 3.1e-120;
0; Mismatches 1;
ERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; SEQ ID NO 180; 1240pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kawai Y,
                                                                                                                                                                                                                                                                                                                                    Human clone PSEC0162 protein, SEQ ID 180.
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                                                                                                                                                          ADY63175 standard; protein; 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-00194179.
2000JP-00118775.
2000JP-00183766.
2000EP-00114090.
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ilarity 99.6%;
Conservative (
                                                                                                                                                                                                                                                                            02-JUN-2005 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 270; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; ADY63174.
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            HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNQK 240
                                                                   HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRPRVTKVEHKSNQK 240
                                                                                                                                                                                                                                                                                                                                                                        Human; sheep; pig; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; blodiversity; gene therapy; nutrition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fly, sea urchin and tomato. These were derived from expressed sequence tags (ESTs) from the organism of interest. They can be used in diagnostics, forensizes, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a protein of the invention
YALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQI
                                                     VHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVCGHHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         solated polypeptide for treatment of diseases, diagnostics, raising
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen R, Asundi V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 811; DB 4; Length 195;
Pred. No. 4.3e-65;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ou P, Qian XB, Wang Z,
Zhang J, Werhman T;
                                                                                                                                                                  ERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
                                                                                                                                                                                  ERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
                                                                                                                                                                                                                                                                                                                                                 Human EST encoded protein SEQ ID NO: 1497.
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                                                                                                                                                                                                                                                                 AAM23972 standard; protein; 195
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17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00631451.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-JAN-2001; 2001WO-US002687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 56.9%;
Best Local Similarity 99.4%;
Matches 157; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhou P,
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Y, Drmanac RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-476164/51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAH98631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 195 AA;
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                                                                                                                                                                  241
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The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating mythoid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents the amino acid sequence of a novel human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                           120
                                                                               61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTEARQDIEEEKVEKIELNDSVNENSDTVGQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; lymphoid cell disorder; lymphoid cell disorder; lissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue replacement; burn; incision; ulcer; cancer; human.
1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPRYIA 60
                                                           61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tang YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA,
Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT,
Haley-Vicente D;
                                                                                                                                                                     VHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGEP 158
                                                                                                                                             121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; SEQ ID NO 830; 156pp; English.
                                                                                                                                                                                                                                                                                             ADI21579 standard; protein; 195 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-SEP-2002; 2002WO-US029964.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-SEP-2001; 2001US-0323739P.
13-SEP-2002; 2002US-00323739.
                                                                                                                                                                                                                                                                                                                                                                                                                             Novel human polypeptide #58.
                                                                                                                                                                                                                                                                                                                                                                                   15-APR-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-354603/33.
N-PSDB; ADI21359.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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The invention relates to nucleic acid sequences (AAV84411 to AAV84633) encoding human secreted proteins (AAW88534 to AAW88756). The secreted protein gene sequences are deposited with the ATCC under deposit numbers ATCC 97979, 97974, 97975, 97977, 209007, 209008, 209009, 209010, 209011, 209080, 209011, 209082, 209011, 209084, 209085, 209011, Host cells comprising recombinant vectors containing the nucleic acid sequences are used for the recombinant production of the secreted proteins. The polynucleotide and amino acid sequences are useful for are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated human genes and the secreted polypeptides they encor
useful for diagnosis and treatment of e.g. cancers, neurological
disorders, immune diseases, inflammation or blood disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 11; Page 511; 772pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-059865/05.
N-PSDB; AAV84456.
       06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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-SEP-1997;
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05-SEP-1997
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                                                                                                                                                                                                                                                      05-SEP-19
05-SEP-19
05-SEP-19
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05-SEP-19
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                                                                                                                                     SEP-1
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                                                                                                                                                                                                                                   05-SEP-
ö
                                                                                                                                                                                                                                                                                                                  Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foctal deficiency; blood; allergy; renal; immune system; asthma; lymphocytic disease; brain; hepatic; Lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; prostate; obseity; osseoclase; thyrus; osteoporosis; arthritis; testis; lung; thyroidtis; thyroid; digestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.
                                                                                                             YALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQI 120
                                                                                                                         61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTEARQDIBEBKVEKIELNDSVNENSDTVGQI 120
                                                                     MAPRALPGSAVIAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA 60
                                                                                 Gaps
                                                 ö
                            7; Length 195;
                            Score 811; DB 7; Length 19
Pred. No. 4.3e-65;
0; Mismatches 1; Indels
                                                                                                                                                       121 VHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSP 158
                                                                                                                                                                  Secreted protein encoded by gene 46 clone HCFMV39.
                                                                                                                                                                                                                                 AAW88579 standard; protein; 103
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97135 - 0048881P
97135 - 0048881P
97135 - 0048881P
97135 - 0048882P
97135 - 0048834P
97135 - 0048834P
97135 - 0048894P
97135 - 0048899P
97135 - 0048899P
97135 - 0048899P
97135 - 0048899P
97135 - 0048891
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97US-0048877P.
97US-0048878P.
97US-0048880P.
                          56.9%;
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                                                                                                                                                                                                                                                                          01-MAR-1999 (first entry)
                        Query Match
Best Local Similarity 99.4
Matches 157; Conservative
       Sequence 195 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        06-JUN-1997;
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06-JUN-1997;
06-JUN-1997;
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06-JUN-1997
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Young P, Greene JM, Ferrie AM, Ruben SM, Rosen CA, Hu J;
Olsen HS, Ebner R, Brewer LA, Moore PA, Shi Y, Florence C;
Florence K, Lafleur DW, MI JJ, Fan P, Wei Y, Fischer CL, Soppet
Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA;
9703-0048970P
9703-0048971P
9703-0048971P
9703-0049974P
9703-0049373P
9703-0049373P
9703-0049373P
9703-0057628P
9703-0057628P
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9703-0057648P
9703-0057668P
9703-0057668P
9703-0057668P
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97US-0057764P.
97US-0057765P.
97US-0057770P.
97US-0057771P.
97US-0057774P.
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encode

us-10-620-562-2.rag

useful for preventing, treating or ameliorating medical conditions e.g.

by protein or gene therapy. Pathological conditions can be also diagnosed
by determining the amount of the new polymeptides in a sample or by
determining the presence of mutations in the new polymucleotides.

Specific uses are described for each of the polymucleotides, based on
which tissues they are most highly expressed in, and include developing
to the disponse or treatment of cancer, neurodegenerative
disporders for the disponse or treatment of cancer, neurodegenerative
disporders, tumours, leukemias, diseases of the immune system, autoimmune
diseases, hepatic and renal disease of the immune system, autoimmune
diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
ischemic shock, Alzheimer's and cognitive disorders involving osteoclasts
such as osteoporosis, arthritis or malignancies, diseases of testes, lung
to thymus, digestive/endocrine disorders, infections and AIDS. The
polypeptides are also useful for identifying their binding partners. The
present sequence represents human secreted protein (see descriptor line
for gene number and clone identification) Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antiinflammatory; immunostimulant; cytostatic; cardiant; vascular; anti-anglogenic; ophthalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; antitparkinsonian; attimicrobial; gene therapy; vaccine; immune disorder; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; parkinson's disease; alzheimer's disease; 1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA 60 1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA 60 1; 33.5%; Score 477.5; DB 2; Length 103; 95.0%; Pred. No. 3.3e-35; ive 0; Mismatches 4; Indels 1. Human secreted protein encoded by gene 46 SEQ ID NO:294. 61 YALVPVFFIMGLFGVLIC-HLLKKKGYRCTTEAEQDIEEEK 100 61 YALVPVFFIMGLFGVLIXPXXXKKKGYRCTTEAEQDIEEEK 101 ABB50346 standard; protein; 103 AA 24-FEB-2000; 2000US-0184836P. 29-MAR-2000; 2000US-0193170P. 21-FEB-2001; 2001WO-US005614 (first entry) Best Local Similarity 95.0 Matches 96; Conservative Sequence 103 AA; W0200162891-A2 Homo sapiens. 30-AUG-2001. 07-FEB-2002 ABB50346; Query Match 셤 ઠ 셤 8

(HUMA-) HUMAN GENOME SCI INC.

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proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in.

Carivities based on the tissues and cells the genes are expressed in.

Carmaple of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; immunostimulant; antiparkinsonian; antimicrobial; antianflammatory; immunostimulant; antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and caucher's disease), cardiovascular diseases (e.g. cancers and caucher's disease), ardiovascular diseases (e.g. cancers and disorders (e.g. corneal graft neovascularisation and diabetic retinopathy), neurological disorders (e.g. Huntington's chorea, Alzheimer's diseases and Parkinson's diseases (e.g. huntington's chemotaxis. ABA83185 to ABA81193 and ABBS03100 represent sequences used in the exemplification of
                                                                                                         ds encoding 207 human secreted polypeptides, useful for diagnosing and/or treating, e.g. cancers, Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; gene therapy; autoimmune disorder; multiple sclerosis; cancer; systemic lupus erythematosus; haematopoietic cell disorder; allergy; agammaglobulinaemia; ataxia telanglectasia; blood coagulation disorder; affibrinogenaemia; thrombocytopenia; graft-versus-host disease; arthritis; affibrinogenaemia; thrombocytopenia; graft-versus-host disease; arthritis; inflammatory condition; ischemia-reperfusion injury; infectious disease; hyperproliferative disorder; purpura; viral infection; regeneration; bacterial infection; ulcer; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.5%; Score 477.5; DB 4; Length 103; 95.0%; Pred. No. 3.3e-35; ive 0; Mismatches 4; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 YALVPVFFIMGLFGVLIC-HLLKKKGYRCTTEAEQDIEEEK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 YALVPVFFIMGLFGVLIXPXXXKKKGYRCTTEAEQDIEEEK 101
                                                                                                                                                                                                   Claim 11; Page 1103-1104; 1533pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABO44603 standard; protein; 103 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-OCT-2003 (first entry)
                                                                                                                                                        and diabetic retinopathy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the present invention
                                            WPI; 2001-625724/72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                 N-PSDB; ABA83239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 103 AA;
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                                                                                                              Nucleic acids
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                                                                                                                                 preventing,
Greene JM;
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Muben SW, Soppet DR, Young PE, Shi Y, Florence KA, Wei Y;
Florence C, Hu J, Li Y, Kyaw H, Fischer CL, Ferrie AW Fan P;
Feng P, Endress GA, Dillox PJ, Carter KC, Brewer LA, Yu G, Zeng Z;
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Human; secreted protein; precerebellin-like protein; neurodegenerative disorder; behavioural disorder; Alzheimer's disease; parkinson's disease; schizophrenia; mania; dementia; paranola; psychosis; autism; immune disorder; infection; inflammation; allergy; liver disorder; hepatoblastoma; jaundice; hepatitis; immunological disorder; AlDS; leukaemia; rheumatoid arthritis; sepsis; acne; psoriasis; cancer.
                                                                                                                                                                                                                                                                                                                                                                             useful for preparing a composition for diagnosing or treating autoimmune disorders e.g. multiple sclerosis and systemic lupus erythematosus; haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia relangiectasia; blood coagulation disorders e.g. afibrinogenaemia and thrombocytopenia; allergy; graft-versus-host disease; inflammatory conditions e.g. ischaemia-reperfusion injury and arthritis; hyperproliferative disorders e.g. cancer and purpura; infectious disease e.g. viral infection and bacterial infection. The polymolocitide or protein can be used to regenerate damaged tissue e.g. ulcers and Alzheimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                         Soppet DR;
                                                                                                                                                                                                                                                                        New isolated protein, useful for preparing a composition for diagnosing or treating cancer, inflammatory, immune or infectious diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA
                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated HEMAE80 protein. The protein is
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                                                                                                                     , Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wai Y, Flacher CL, So
Feng P, Dillon PJ, Endress GA,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human protein from novel secreted protein gene 46.
                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 294; 172pp; English.
                                                                                                                    Ferrie AM,
Brewer LA, 1
DW, Ni J, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABO26083 standard; protein; 103
98WO-US011422.
98US-0092921P.
98US-0094657P.
98US-00205258.
                                                                                   (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 95.0
                                                                                                                    Young P, Greene JM,
Olsen HS, Ebner R, B
Florence K, Lafleur D
Li Y, Zeng Z, Kyaw H
                                                                                                                                                                                                                       WPI; 2003-540804/51.
N-PSDB; ACH04740.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 103 AA;
                15-JUL-1998;
30-JUL-1998;
04-DEC-1998;
   04-JUN-1998;
                                                                                                                                                                                       Carter KC;
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Matches
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ABO26083
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Homo sapiens US6525174-B1

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97US-0048875P.
97US-0048877P.
97US-0048877P.
97US-0048810P.
97US-0048881P.
97US-0048881P.
97US-0048881P.
97US-0048881P.
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9705-0048894P
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                    98US-00205258
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
       25-FEB-2003
                                                                                                                                                         06-JUN-1997
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The invention relates to an isolated protein comprising amino acid residues 33-205 or 1-205 of a a novel human secreted protein appearing as ABO2525. The protein is encoded by one of 238 disclosed CDNA sequences encoding 238 secreted proteins. ABD26252 is a precerebellin-like protein. Also included are a composition comprising the protein and a carrier and an isolated protein produced by expressing the protein cited above by a cell, and recovering the protein. The protein for diagnosing or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, chemitia, paranola, psychoses or autism), immune disorders (e.g. Alzheimer's infection, inflammation, allergy), liver disorders (e.g. ADDS, leukaemia, rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present requence is one of the 238 disclosed novel secreted proteins. Note: The sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data for this patent did not form part of the printed sequence data secreted broteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soppet DR;
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dermatological; immunosuppressive; antiinflammatory; immunostimulant;
cytostatic; cardiant; vascular; anti-angiogenic; ophthalmological;
neuroprotective; nootropic; anticonvulsant; antialzheimers; vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Gaps
                                                                                                                                                                                                                                                                                                                                               New precerebellin-like protein, useful for diagnosing or treating neurodegenerative and behavioral disorders, immune disorders, liver disorders, and cancer.
                                                                                                                                                                                             Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wei Y, Fischer CL, SO
Feng P, Dillon PJ, Endress GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Length 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 294; 156pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB50685 standard; protein; 181 AA
                                                                                                                                                                                           , Ferrie AM,
Brewer LA,
r DW, Ni J,
                                                                                                                                                                                                                                                   Yu G,
             97US-0057776P.
97US-0057777P.
97US-0057777P.
98WO-US011422.
98US-0092921P.
                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC.
97US-0057775P
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                                                                                                                                                                                             Young P, Greene JM,
Olsen HS, Ebner R, B
Florence K, Lafleur Di
Li Y, Zeng Z, Kyaw H
Carter KC;
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N-PSDB; ACD44550.
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              05-SEP-1997
05-SEP-1997
                                                  05-SEP-1997
18-DEC-1997
                                                                                     04-JUN-1998
15-JUL-1998
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Matches
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AAE20965 standard; protein; 181 AA.

AAB20965

01-JUL-2002

AAE20965;

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proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in.

Example of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; immunostimulant; anti-HV; cytostatic; cardiant; anti-angiogenic; optibalmological; cardiant; anti-angiogenic; optibalmological; neuroprotective; noctropic; anticonvulsant; antialzheimers; vascular; antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used in the prevention, diagnosis and treatment of immune disorders (e.g. multiple prevention, diagnosis and treatment of immune disorders (e.g. multiple sclerosis, systemic lupus erythematous and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and canchers disease), cardiowascular diseases (e.g. Scinntar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. conceal graft neovascularisation and disbetic cationpathy), neurological disorders (e.g. Humtington's chonces, Alzheimer's disease and Parkinson's diseases), cardiomyopathy and coronary arteriosclerosis), angiogenic cetinopathy, neurological disorders (e.g. Humtington's chorces, Alzheimer's disease and Parkinson's diseases), cardiomyopathy, regeneration and/or chemotaxis. ABA83185 to the promoting wound healing, regeneration and/or chemotaxis. ABA83185 to the armonial dispense used in the exemplification of
antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis; Chaga's cardiomyopathy; coronary arteriosclerosis; angiogenic disorder; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Moore PA, Olsen HS, Rosen CA;
PE, Shi Y, Florence KA, Wei Y;
waw H, Fischer CL, Ferrie AM, Fan P;
PJ, Carter KC, Brewer LA, Yu G, Zeng Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kyaw H, Fischer Cy. P.T. Carter KC,
                                                                                                                                                                  Parkinson's disease; infectious disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Soppet DR, Young C, Hu J, Li Y, Kyaw H,
                                                                                                                                                                                                                                                                                                                                                                                              24-FEB-2000; 2000US-0184836P.
29-MAR-2000; 2000US-0193170P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                   21-FEB-2001; 2001WO-US005614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  diabetic retinopathy.
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Florence C, Hu o,
Endress GA,
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                                                                                                                                                                                                                                                        WO200162891-A2.
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                                         97 EEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG 156
                                                      Gaps
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  Length 181;
                      8; Indels
Score 332; DB 4;
Pred. No. 1.1e-21;
                     3; Mismatches
                                                                                     SPPVSPGPLSPGGTPG 172
 23.3%;
85.5%;
                      65; Conservative
            Local Similarity
                                                                                     157
 Query Match
                     Matches
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Human; tumour necrosis factor receptor; TNP; TR21; TR22; immune disorder; autoimmune haemolytic anaemia; rheumatoid arthritis; Addison's disease; allergy; cancer; ulcerative colitis; cardiovascular disorder; epilepsy; myocardial ischaemia; wound healing; neurological disease; infection; cerebral anoxia; gene therapy; immunosuppressive; antiproliferative; cytostatic; cardiant; vasotropic; neuroprotective; antibacterial; virucide; fungicide; nootropic; ophthalmological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors, TR21 and TR22 and polyhucleotides encoding them. Sequences of the invention are useful in the diagnosis, treatment and prevention of sancers (e.g., cancers of the adrenal gland, bone, urogenital or bone marrow, in particular breast and ovarian cancer), immune disorders (e.g., autoimmune haemolytic anaemia, rheumatoid arthritis, allergies, Addison's disease, ulcerative colitis), cardiovascular disorders (e.g., myocardial ischaemias), wound healing, neurological diseases (e.g., cerebral anoxia, epilopsy) and infections diseases such as viral, bacterial, fungal and parasitic infections. They are also useful in gene therapy. The present sequence is human TR21 protein fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel human tumour necrosis factor (TNF)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Two novel proteins, TR21 and TR22, which are members of the tumor necrosis factor receptor, useful for the diagnosis and treatment of immune disorders, cancer, cardiovascular disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23.3%; Score 332; DB 5; Length 181; 85.5%; Pred. No. 1.1e-21; tive 3; Mismatches 8; Indels
                                                                                Human TR21 receptor protein fragment.
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 5; 248pp; English.
                                                                                                                                                                                                                                                                                                                       label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                           label= Unknown
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                                                                                                                                                                                                                                                                                                                                                                          Misc-difference 60
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                                                                                                                                                                                                                                                       Homo sapiens
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Conservative

65,

Matches

Local Similarity

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Gaps

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SPPVSPGLCHQGGRQG 151

RESULT 12

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Human; gene therapy, autoimmune disorder; multiple sclerosis; cancer; systemic lupus erythematosus; haematopoietic cell disorder; allergy; agammaglobulinaemia; ataxia telangiectasia; blood cosgulation disorder; afbirinogensemia; thrombocytopenia; graft-versus-host disease; arthritis; inflammatory condition; ischaemia-reperfusion injury; infectious disease; hyperproliferative disorder; purpura; viral infection; regeneration; bacterial infection, ulcer; Alzheimer's disease.
76 KKKKVEKKXLINDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG 135
                                                                                                                                                                                                                                                          Novel human secreted protein #46 fragment #2.
                                                                                                                                                            ABO44942 standard; protein; 181 AA.
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97US-0048877P.
97US-0048878P.
97US-0048881P.
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97US-0048882P.
97US-0048882P.
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97US-0048963P.
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9705-0049019P-
9705-0049373P-
9705-0049375P-
9705-0057584P-
9705-0057624P-
                                                                   SPPVSPGLCHQGGRQG 151
                                                  SPPVSPGPLSPGGTPG 172
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06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
06-JUN-1997;
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05-SEP-1997;
05-SEP-1997;
05-SEP-1997;
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06-JUN-1997;
06-JUN-1997;
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ABOUT 113
ABOUT 120
ABOUT ABOUT 120
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Ruben SM,
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9703-0057634P

9703-0057634P

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             05-SEP-1997;
05-SEP-1997;
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, Ruben SM, Rosen CA, Hu J;
Moore PA, Shi Y, Florence C;
Fan P, Wei Y, Fischer CL, Soppet DR;
Peng P, Dillon PJ, Endress GA; Brewer LA, DW, Ni J, H, Yu G, Young P, Greene JM, 1 Olsen HS, Ebner R, B: Florence K, Lafleur Di Li Y, Zeng Z, Kyaw H Carter KC,

WPI; 2003-540804/51.

New isolated protein, useful for preparing a composition for diagnosing or treating cancer, inflammatory, immune or infectious diseases.

Disclosure; Page 28; 172pp; English.

useful for preparing a composition for diagnosing or treating autoimmune disorders e.g. multiple solerous and systemic lupus erythematosus; thaematopoietic cell disorders e.g. agammaglobulinaemia and ataxia telangieccasia; blood coagulation disorders e.g. afibrinogenaemia and thrombocycopenia; allergy; graft-versus-host disease; inflammatory conditions e.g. ischaemia-reperfusion injury and arthritis; orginal infection and bacterial infection. The polymuclectide or protein can be used to regenerate damaged tissue e.g. ulcers and Alzhaimer's disease. The present sequence represents the amino acid sequence of a novel human secreted protein fragment. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format directly from USPTO at The invention relates to an isolated HEWAE80 protein. The protein is

Sequence 181 AA;

Query Match

23.3%; Score 332; DB 6; Length 181;

us-10-620-562-2.rag

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                      97 EEEKVEKIELINDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG 156
                               KKKKVEKXXLADSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPYTPSTPG 135
                                                                                                                                                               Secreted protein; precerebellin-like protein; sepsis; acne; psoriasis; neurodegenerative disorder; behavioural disorder; Alzheimer's disease; Parkinson's disease; Buntington's disease; schizophrenia; mania; dementia; paranoia; psychosis; autism; immune disorder; infection; inflammation; allergy; liver disorder; heparoblastoma; jaundice; hepartitis; immunological disorder; AIDS; leukaemia; rheumatoid arthritis;
          Gaps
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                                                                                                                                                 Protein associated with novel secreted protein gene 46 #2.
        8; Indels
85.5%; Pred. No. 1.1e-21;
ive 3; Mismatches 8
                                                                                                     ABO26422 standard; protein; 181 AA.
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97US-0048877P
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       Conservative
Similarity
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Best Local
Matches 6
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97US-0057778P
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(HUMA-) HUMAN GENOME SCI INC

Soppet DR; Ruben SM, Rosen CA, Hu J; Moore PA, Shi Y, Florence C, Pan P, Wei Y, Flacher CL, Soy Feng P, Dillon PJ, Endress GA; Ferrie AM, Brewer LA, DW, Ni J, ξ Yu G, Young P, Greene JM, Olsen HS, Ebner R, B Florence K, Lafleur Di Li Y, Zeng Z, Kyaw H Carter KC;

WPI; 2003-511926/48.

New precerebellin-like protein, useful for diagnosing or treating neurodegenerative and behavioral disorders, immune disorders, liver disorders, and cancer.

Disclosure, Col 52; 156pp; English.

The invention relates to an isolated protein comprising amino acid residues 33-205 or 1-205 of a novel human secreted protein appearing as ABO26252. The protein is encoded by one of 238 disclosed cDNA sequences encoding 238 secreted proteins. ABO26252 is a precerebellin-like protein. Also included are a composition comprising the protein and a carrier and a isolated protein produced by expressing the protein and a carrier and cell, and recovering the protein. The proteins are useful for disgnosing or treating neurodegenerative and behavioural disorders (e.g. Alzhelmer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranola, psychoses or autism), immune disorders (e.g. Alzhelmer's infection, inflammation, allergy), ilver disorders (e.g. hepatoblastoma, rheumatoid arthritis, sepsis, acne, psoriasis) and cancer. The present sequence is a protein associated with one of the 238 disclosed novel

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206 VQTS---HRPVSKLPPAPPNVP--HICPHRHHLHTVQGLASLSGPCCSRCSQKKWPEVLL 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 382 AA;
                                                                                                                                                                                                                                                                                                   Williams LT,
Halenbeck RF,
                                                                                                 02-MAY-2003;
02-MAY-2003;
19-MAY-2003;
19-MAY-2003;
                                                                                                                                                            09-JUN-2003;
08-JUL-2003;
08-JUL-2003;
                                                                  18-APR-2003;
                                                                                                                                    22-MAY-2003;
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                                                                 KKKKVEKXKINDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG 135
                                                                                                                                                                                                                      Cytostatic; Antiinflammatory; Immunosuppressive; Antibacterial; Virucide; cancer; inflammatory; immune; human secreted protein.
                                                      97 EEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG
                                        Gaps
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                       Length 181;
                                       8; Indels
                      Score 332; DB 7;
Pred. No. 1.1e-21;
3; Mismatches 8;
                                                                                                                                                                                                      Human secreted protein SEQ ID #220.
                                                                                                                                                   ADP29453 standard; protein; 382 AA
                                                                                                                                                                                                                                                                                                                 29-AUG-2002; 2002US-0406576P.
29-AUG-2002; 2002US-040658P.
29-AUG-2002; 2002US-040658BP.
29-AUG-2002; 2002US-040668BP.
29-AUG-2002; 2002US-040661P.
29-AUG-2002; 2002US-040661P.
29-AUG-2002; 2002US-040661P.
29-AUG-2002; 2002US-040664P.
29-AUG-2002; 2002US-040664P.
29-AUG-2002; 2002US-040664P.
29-AUG-2002; 2002US-040665P.
29-AUG-2002; 2002US-040665P.
29-AUG-2002; 2002US-040665P.
29-AUG-2002; 2002US-040666F.
17-SEP-2002; 2002US-040666F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-2002; 2002US-0410949F.
17-SEP-2002; 2002US-0410949P.
17-SEP-2002; 2002US-0410953F.
17-SEP-2002; 2002US-0410953F.
17-SEP-2002; 2002US-0410958F.
17-SEP-2002; 2002US-0410959F.
17-SEP-2002; 2002US-0410961P.
17-SEP-2002; 2002US-0410961P.
17-SEP-2002; 2002US-04110961P.
17-SEP-2002; 2002US-0411019P.
                                                                                        SPPVSPGPLSPGGTPG 172
                                                                                                       SPPVSPGLCHQGGRQG 151
                      23.3%;
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17-SEP-2002; 2002US-0411024P
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                                                                                                                                                                                                                                                                                                  28-AUG-2003; 2003WO-US026780
                                                                                                                                                                                    (first entry)
                                      65; Conservative
                              Best Local Similarity
     Sequence 181 AA
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94 ----QDIEEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESP 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to an isolated nucleic acid molecule encoding a polypeptide which is believed to be cycostatic, antiinflammatory, immunosuppressive, antibacterial and virucidal. The composition and methods are useful for diagnosing, preventing and treating diseases such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases. The present sequence represents a human secreted protein. The present sequence is available on WIPOWEB and is not in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       162 GGGGSGTED------ANEDTIGVLVRLITEKKENAAALEELLKE---YHSKQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44 TPSPSNDTGNGHPE----YIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New nucleic acid molecule for diagnosing, preventing or treating dise such as proliferative (e.g. cancer), inflammatory, immune, metabolic, genetic, bacterial and viral diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hestir K, Beaurang PA, Behrens D;
hakota S, Haishan L, Linnemann T;
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Halenbeck RF, Huang MM, Kothakota S, Haisha
Pierce K, Wang Y, Wong JGP, Wu G, Zhang H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1451; 428pp; English.
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2002US-0411055P
2002US-041101P
2002US-041111P
2002US-0411111P
2003US-0463710P
2003US-0463716P
2003US-0463716P
2003US-0463716P
2003US-0467201P
2003US-0467201P
2003US-0467201P
2003US-047130F
2003US-048523BF
2003US-048523BF
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Search completed: February 23, 2006, 12:03:53 Job time : 190 secs
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Sequence 1672, Ap
Sequence 104, App
Sequence 22, Appl
Sequence 62, Appl
Sequence 62, Appl
Sequence 14, Appl
Sequence 287, Ap
Sequence 266, Appl
Sequence 266, Appl
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Sequence 4, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 131, App
Sequence 2203, Ap
Sequence 67, Appli
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Sequence 67, Appli
Sequence 67, Appli
                                                                               February 23, 2006, 12:09:38; Search time 18 Seconds (without alignments) 224.136 Million cell updates/sec
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Sequence 2
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1 MAPRALPGSAVLAAAVFVGG.....ETVNGEVPATPVKRERSGTE
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1. /cgn2_6/ptodata/1/pubpaa/USO8 NEW PUB.pep:*
2. /cgn2_6/ptodata/1/pubpaa/USO6 NEW PUB.pep:*
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5: /cgn2_6/ptodata/1/pubpaa/NSO3 NEW PUB.pep:*
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GenCore version 5.1.7 (c) 1993 - 2006 Biocceleration Ltd
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US-11-198-819-8
US-11-198-819-8
US-10-485-517-131
US-10-485-517-131
US-11-075-512-2203
US-11-075-512-2452
US-11-075-512-2452
US-11-05-232-62
US-11-169-232-62
US-11-169-232-632
US-11-169-232-632
US-11-169-232-632
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US-11-124-877A-268
US-10-714-887-126
US-10-714-887-122
US-11-052-554A-229
US-11-087-100-2
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Length 430;

21.5%; Score 307; DB 7; ilarity 31.0%; Pred. No. 5.7e-21; Conservative 36; Mismatches 69

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522, App
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Fublication No. US20060024267A1
GENERAL INFORMATION:
APPLICANT: Welcher, Andrew A
APPLICANT: Welcher, Andrew A
APPLICANT: Beedigheimer, Michael J
APPLICANT: Boedigheimer, Michael J
APPLICANT
                                                                                                                           US-11-126-313-31

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US-11-124-367A-444

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US-11-124-367A-446

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YOSHIKAWA, TSUTOMU
OTSUKA, MOTOYUKI
NAGAHARI, KENJI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        t TYPE: PRT
CORGANISM: Homo sapiens
US-11-072-512-2688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ઠ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 304 RCSQK-WPEVLLSPEAAAATTPAPTLLPTASRAPKASAKPGRQGEITILSVGRFRVARIP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86 YRCTTEAEQDIEE----EKVEKIELNDSVNENSDTVGQIVHYIMKNEANA----DVLKAM 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           138 VADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVC--GHHLHTVGGV--VERDVCH 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 RCRHKRWHFI------KPT---NKSR----ESRPRRGGEVTVLSVGRFRVTKVE 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31 NGSSRTLHSRTETTPSPSNDTGNGHPE----YIAYALVPVFFIMGLFGVLICHLLKKKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61; Gaps
                                                                                                                                             Sequence 4, Application US/11042814

Publication No. US20060024267A1

GENERAL INCRNATION:

APPLICANT: Welcher, Andrew A

APPLICANT: Welcher, Andrew A

APPLICANT: Boodigheimer, Michael J

APPLICANT: Boodigheimer, Michael J

APPLICANT: Boodigheimer, Michael J

APPLICANT: Boodigheimer, Michael J

APPLICANT: Boun TUNENTON: TNFT/OFG-LIKE MOLECULES AND USES THEREOF

FILE REFERENCE: 01017/36654

CURRENT APPLICATION: TWEPFORD: 0205-01-25

PRIOR PILING DATE: 2005-01-25

PRIOR PLING DATE: 2000-05-15

PRIOR FILING DATE: 2000-01-28

NUMBER OF FILING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE PATENTING DATE: 2000-11-28

SOFTWARE PATENT ON TOWER TOWE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
20.7%; Score 295.5; DB 7; Length 436;
Best Local Similarity 30.6%; Pred. No. 6.8e-20;
Matches 82; Conservative 36; Mismatches 89; Indels 61
-- PEQRISSMVSEVKTITEAGPSWGDLPDSP 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    235 HKSNQKERRSLMSVSGAETVNGEVPATP 262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2688, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ISHII, SHIZUKO
XAMAMOTO, JUN-ICHI
ISONO, YUUKO
HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IRIE, RYOTARO
TAMECHIKA, ICHIRO
SEKI, NAOHIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-11-072-512-2688
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LENGTH: 436
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60 AYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTV-G 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 AEAPQTIDSPITKVQKDPSIKPVTPSPSKLVTSPQSEPPAPFP-PPRSTSSPYHAGNLLQ 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       286 ------RHPTNW--TKPTSPTRSTBABSVLHSEGSRRAADAKPKRW--ISFK 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167 QIVASIQPPQSPPETPQSGPKACSVEELYAIPPDADVAKSTPKSTPVRPKSLFTSQPSGE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    145 -----DPB-SPVTPS----TPGSPPVSPGPLSPGGTPGKHVCGHHLH 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ---SRTETTPSPSNDTGNGHPEYI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 QIVHYIMKNEA-----VADNSLY----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87; Indels 153; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/11198819
; Sequence 6, Application US/11198819
; bubilcation No. US20050287582A1
; GENERAL INFORMATION:
; APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
; COMPUTER: READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC Compatible
COMPUTER: Datentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: PALOAUG-2005
; CLASSIFICATION DATE:
; APPLICATION DATE:
; FILING DATE: US/11/198,819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  328 SFFRRKTDEEDDKEKEREKGKLVGLDG--TVIHMLPPPPVQRHHWFTE 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              224 SVGRFRVTKVE-HKSNQKERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.8%; Score 97.5; DB 7; Length 447; Best Local Similarity 20.6%; Pred. No. 0.18; Matches 72; Conservative 37; Mismatches 87; Indels 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  182 TVGGVVERDVCHRCRH-KRWHFIKPTNKSR-----
FILLE OF INVENTION: Navel full length CDNA FILLE OF INVENTION: Novel full length CDNA FILE REFERENCE: 084335-0191

FILE REFERENCE: 084335-0191

CURRENT APPLICATION NUMBER: US 60/350,978

PRIOR APPLICATION NUMBER: US 60/350,978

PRIOR APPLICATION NUMBER: UP 2001-379298

PRIOR APPLICATION NUMBER: JP 2001-379298

PRIOR PILING DATE: 2001-11-05

NUMBER OF SEQ ID NOS: 4096

SOFTWARE: PATENTIN VET. 2.1

SOFTWARE: PATENTIN VET. 2.1
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US-10-485-517-131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 TTEAEQDIEEEKVEKIELN---DSVNENSDTVGQIVHY-IMKNEANADVLKAMVADNSLY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----CRHKRWHFIK---PTNKSRESRPRRQGEVTV----LSVGRFRVTKVEHKSNQKER 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     145 DPESPVT-PSTPGSPPVSP-----GPLSPGGTPGKHVCGHHLHTVGGV-VERDVCHR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 SRILHSRIETTPSPSNDIGNGHPBYIAYALVPV----FFIMGLFGVLICHLLKKKGYRC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 AQTIHTQEEDLPRPSISAEPG-----TVIPLGSHVTFVCRGPVGVQTFRLERES--RS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/11198819
Publication No. US20050287582A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSER: DARK Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 6.8%; Score 97; DB 7; Length 287; Best Local Similarity 22.7%; Pred. No. 0.11; Matches 58; Conservative 45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/198,819
PRIOR APPLICATION DATA:
APPLICATION WUMBER:
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-WARCH-1997
PRIOR APPLICATION DATA: 06-0033,181
PRIOR APPLICATION DATA: US-00/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATORNEY AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REGISTRATION NUMBER: DX0670K
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
TELECOMMUNICATION INPORMATION:
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                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 287 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein US-11-198-819-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Palo Alto
STATE: California
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126 GPDSPDTEPGSSAGPTQRPSDNSHNEHAPASQG-----LKAEHLYILIGVSVVFLFCLL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89 ITEAEQDIEEEKVEKIELN---DSVNENSDTVGQIVHY-IMKNEANADVLKAMVADNSLY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 DPESPVT-PSTPGSPPVSP-----GPLSPGGTPGRHVCGHHLHTVGGV-VERDVCHR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 SRILHSRIETTPSPSNDTGNGHPEYIAYALVPV----FFIMGLFGVLICHLLKKKGYRC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 AQTIHTQEEDLPRPSISAEPG-----TVIPLGSHVTFVCRGPVGVQTFRLERES--RS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6.8%; Score 97; DB 7; Length 287; 22.7%; Pred. No. 0.11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US200502562991
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: University of Sheffield
APPLICANT: Biosynexus Incorporated
APPLICANT: Bester, Simon
APPLICANT: Poster, Simon
APPLICANT: Poster, Simon
APPLICANT: Poster, Simon
APPLICANT: PROSTER, 2004-02-02
CURRENT APPLICATION NUMBER: US/10/485,517
CURRENT FILING DATE: 2004-02-02
FRIOR APPLICATION NUMBER: GB 0118825.9
FRIOR FILING DATE: 2001-08-02
FRIOR FILING DATE: 2002-1-09
NUMBER: OF SEQ ID NOS: 424
SEQ ID NO 131
                                                               PALLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DXC
TELECOMMUNICATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243 RSLMSVSGAETVNGEV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 SALAAGSSQEVTYAQL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (650)496-1204
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:
ELENGTH: 287 amino acids
04-AUG-2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 287 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best_Local Similarity 22.79
Matches 58; Conservative
                        CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein
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108 PKIILVIGGPGSGKGTQSLKIAERYGPQYISVGELLRKKIHSTSSNRKWSLIAKIITTGE 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PGSPPVSPGPLSPGGTPGKHVC---GHHLHTVGGVVERDVCHRCRHKRWHFIKPTNKSRE 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53 NGHPEYIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEE-----EKV---- 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 EKIELNDSVNENSDTV----GQIVHYIMKNEANADVLKA--MVADNSLYDPESPVTPST 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 NDAKEYLARREIPQLF-ESLINGLMC-----SKPEDPVEYLESCLOKVKELGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40; Gaps
       310 HRAH-----YDLRHTFMGVVSLGSPSGEVSHPRKTRTVVQPSVG 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 7; Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 76; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 67, Application US/11240769; Sequence 67, Application US/20060036089A1; September 1 Publication No. US20060036089A1; APPLEANT: Soppet et al.; TITLE OF INVENTION: 33 Human Secreted Proteins; FILE REFERENCE: PZ037PLC2; CURRENT APPLICATION NUMBER: US/11/240, 769; CURRENT FILING DATE: 2005-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
6.0%; Score 85; DB 7
Best Local Similarity 20.6%; Pred. No. 1.1;
Matches 40; Conservative 38; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: TAMECHIKA, ICHIRO
APPLICANT: SEKI, NAOHIKO
APPLICANT: SOSHIKAWA, TSUTOMU
APPLICANT: OTSUKA, MOYOVUKI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KENJI
APPLICANT: NAGAHARI, KONJI
APPLICANT: NASUHO, YASUHIKO
APPLICANT: NASUHO, NOVEL FULL REFERENCE: 084335-0191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/11/072,512
CURRENT FILING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
PRIOR FILING DATE: 2002-01-25
PRIOR APPLICATION NUMBER: JP 2001-379298
PRIOR PILING DATE: 2001-11-05
NUMBER OF SEQ ID NOS: 4096
SOFTWARE: PATENTIN Ver. 2.1
                                                                                                                   Sequence 2203, Application US/11072512
Publication No. US20060029945A1
                                                                                                                                                                                APPLICANT: 1SOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOXASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: SATO, HIROYUKI
APPLICANT: SATO, HIROYUKI
APPLICANT: ISHII, SHIZUKO
APPLICANT: YAMAMOTO, JUN-ICHI
APPLICANT: ISONO, YUUKO
APPLICANT: HIO, YUKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 SRPRRQGEVTVLSV 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             168 LAPQ---ÈTTITEI 178
                                                                                                                                                                                                                                                                                                                                                                                        OTSUKA, KAORU
NAGAI, KEIICHI
IRIE, RYOTARO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                GENERAL INFORMATION:
                                                                                              JS-11-072-512-2203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-11-072-512-2203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 2203
LENGTH: 241
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Sequence 6, Application US/1088962

Publication No. US20050266531A1

GENERAL INPORMATION:

APPLICANT: Saint Louis University

APPLICANT: Ray, Rannit

APPLICANT: Ray, Rannit

APPLICANT: Basu, Arma

TITLE OF INVENTION: Growth

TITLE OF INVENTION: Growth

TITLE OF INVENTION: 213 PCT

CURRENT APPLICATION NUMBER: US/10/888,962

CURRENT PILING DATE: 2004-07-09

PRIOR APPLICATION NUMBER: 06/487,126

PRIOR APPLICATION NUMBER: 06/487,126

NUMBER OF SEQ ID NOS: 15

SOFTWARE: Patentin version 3.2

SEQ ID NO 6

LENGTH: 367
                                                                                                                                                                                                                                                                                                                                                                                        135 KAMVADNSLYDPESPVTPSTPGSP------PVSPGPLSP--GGTPGKHVCGHH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 LHTVGGVVERDVCHRCRHKRWHFIKPTNK--SRESRPRRQGEVT--VLSVGRFRVTKVEH 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 CHLLKKKKGYRCTTE-AEQDIEBEKVE-KIELNDSVNENSDTVGQIV-HYIMKNEANADVL 134
                                                                                                                                                                                                                                                                                                                             127 NEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGT-PGKHVC----GHHL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75 V-----LICHLLKKKGYR-CTTEAEQDIEEEKVEKIELNDSVNENSDTVGQIVHYIMK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262 EGANEAV------PTPVVDPDAPSPPLGAPGLPPAGSPPDSHVLLAAPPGHQL 309
                                                                                                                                                                                                        26 LVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEY-----IAYALVPVFFIMGLFGVLI 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25 PLVAPDNGSSRTLHSRTETTP--SPSNDTGNGHPEYIAYA-LVPV-----FFIMGLFG 74
                                                                                                                                                                                                                                      818 PPIV-----PPTPPTPEVPSEPETPTPPTPEVPSEPETPTPEVPTEPGKP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53; Gaps
                                                                                                                                                                  Gape
                                                                                                                                                             81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 6.0%; Score 85.5; DB 6; Length 367; Best Local Similarity 25.6%; Pred. No. 1.8; Matches 58; Conservative 23; Mismatches 93; Indels 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 HTVGGVVERDVCHRCRHKRWHFIKPTNKSRE-SRPRRQGEVTVLSVG 226
                                                                                                                   Length 948
                                                                                                                                                             94; Indels
                                                                                                              #; Score 87.5; DB 6;
#; Pred. No. 4.4;
30; Mismatches 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 KSNQKERRSLMSVSGAETVN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   903 KKAQSKKSELPETGGEESTN 922
                                               ; ORGANISM: Staphylococcus aureus US-10-485-517-131
                                                                                                              Query Match
Best Local Similarity 21.2%;
Matches 55; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----- 998
LENGTH: 948
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-888-962-6
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124 IMK--NEANADVLKAMVAD--NSLYDPESPVTPSTPGSPPV-----SPGPLSPGGTPGK 173
                                                                                                          ::: :: :| | | : : : | | | 845 LVESMDDTDADSLKSARAEHLISTLEDPVAVVLGSSPEKDKVSLVAAFSPGVVSLGVQAGK 904
                                                                                                                                                                    174 HV-----CG 177
                                                                                                                                                                                                                  905 FIGPIAKLĊĠ 914
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APPLICANT:
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                                                                        ઠે
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (213)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-11-240-769-67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59 IAYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | ::| |||: |: | ||1
183 IINSVVVVFFLSGILSMIIIRTLRK-------DIANYXKED-DIEDTMEESG--W 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGG-----T 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (164)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 PGKHVCGH-----HLHT----VGGVVERDVCHRCRHKRW----HFIXPTNKS 209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 31, Application US/10467962B

Publication No. US2000246784A1

GENERAL INFORMATION:

APPLICANT: Pleach, Gunnar

APPLICANT: Pleach, Gunnar

APPLICANT: Baeschner, Klaus

APPLICANT: Daeschner, Klaus

APPLICANT: Mathieu

TITLE OF INVENTION: Identification of Herbicidally Active Substances

FILE REFERENCE: 2000 857

CURRENT APPLICATION NUMBER: US/10/467,962B

CURRENT FILING DATE: 2003-08-14

PRIOR APPLICATION NUMBER: PCT/EP02/01466

PRIOR PILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 109

SOFTWARE: PatentIn Vers. 2.0

SEQ ID NO 31

LENGTH: 954
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   210 RESRPRRGGEVIVLSVGRFRVTKVE--HKSNOKERRSLMSVSGAETVN--GEVPA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 VEERSLLYGN-SVPWCGFWHILRIELLHIGKALIRSGALSHHGGSAVHVVRDLPA 362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 6.0%; Score 85; DB 7; Length 377; Best Local Similarity 22.6%; Pred. No. 2.1; Matches 53; Conservative 28; Mismatches 66; Indels
PRIOR APPLICATION NUMBER: 09/997,131
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2001-11-30
PRIOR FILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-07-28
PRIOR PILING DATE: 2000-02-08
PRIOR APPLICATION NUMBER: 60/119,468
PRIOR PILING DATE: 1999-02-10
NUMBER OF SEQ ID NOS: 173
SEQ ID NO 67
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                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE
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69 IMGLFGVLICHLLK---KKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQIVHYIM 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           724 KD--NADLLSPLKKWKSRYLMEQNVTKLLRPLSPVTPPPPNSGSKSPQLATPGSSHPGEE 781
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 VLAAAV-FVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGH-PEYIAYALVPVFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            74; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 5.9%; Score 84; DB 7; Best Local Similarity 24.9%; Pred. No. 15; Matches 53; Conservative 26; Mismatches 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | | : : : : | | | ECRNGYSLMPSPVTSLTTASRCNTPLQPELCHR 814
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: STANDALIANO, ALDIANO, APPLICANT: SEKI, NAOHIKO
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: YOSHIKAWA, TSUTOMU
APPLICANT: NAGAHARI, KENJI
APPLICANTON: NOVel full length CDNA
FILE REFERENCE: 0862-03-07
CURRENT PLING DATE: 2005-03-07
PRIOR APPLICATION NUMBER: US 60/350,978
SEQ ID NO 2452
LENGTHER OF SEQ ID NOS: 4096
SEQ ID NO 2452
LENGTHER OF SEQ ID NOS: 4096
SEQ ID NO 2452
Sequence 2452, Application US/11072512
Publication No. US20060029945A1
GENERAL INFORMATION:
                                                                                           APPLICANT: ISOGAI, TAKAO
APPLICANT: SUGIYAMA, TOMOYASU
APPLICANT: OTSUKI, TETSUJI
APPLICANT: WAKAMATSU, AI
APPLICANT: SATO, HIROYUKI
                                                                                                                                                                                                                                                   ISHII, SHIZUKO
YAMAMOTO, JUN-ICHI
ISONO, YUUKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAMECHIKA, ICHIRO
                                                                                                                                                                                                                                                                                                                                        HIO, YURI
OTSUKA, KAORU
NAGAI, KEIICHI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97 EEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTP--ST 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52 GNGHPEYIAYALVPVFFIM----GLFGVLICH------LLKKKGYRCTTEAEQDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               5.8%; Score 82.5; DB 6; Length 399; 25.4%; Pred. No. 3.9;
Sequence 1672, Application US/10467657

Publication No. US20050260581A1

GENERAL INFORMATION:

APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita

APPLICANT: PONTANA Maria Rita

APPLICANT: MASIGNANI Vega

APPLICANT: MONACI Eliasbetta

TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS

FILE REFERENCE: 2003-08-11

PRIOR APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11

PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR PAILNG DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218

SOFTWARE: SEQ WIN99, version 1.04

SEQ ID NO 1672

LENGTH: 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 104, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION:
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Genetics Institute, Inc. STREET: 87 CambridgePark Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Neisseria gonorrhoeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
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COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 370 QGHPEASPGPQDVG 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
Matches 34; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-467-657-1672
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US-11-169-232-104
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93 KKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQI--VHYIMKNEANADVLKAM-VA 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                202 DNKKNRTKKKPTPKPPVVDEAGSG-LDNGDPKVTTPDTSTTQHNKVSTSPKITT---- 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----AKPIN-PRPSLPPNSDTSKETSLTVNKETTVETKETTTTNKQTSTDGKEKTTS 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23 SSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIAYALVPVFFIMGLFGVLICHLLK 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 52, Application US/11169232
Publication No. US20060025570A1
GENERAL INFORMATION: Katherine
APPLICANT: Turner, Katherine
Clark, Stephen C.
Jacobs, Kenneth
Hewick, Rodney M.
Gener, Thomas G.
TITLE OF INVENTION: Megakaryocyte Stimulating Factors
NUMBER OF SEQUENCES: 143
CORRESPONDENCE ADDRESS:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 RHKRWHFIKPTNKSRESRPRROGEVTVLSVGRFRVTKVEHK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 5.8%; Score 82.5; DB 7; Best Local Similarity 20.1%; Pred. No. 17; Matches 55; Conservative 35; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           239 QKERRSLMSVSGAETV-NGEVPATPVKRERSGTE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | | : | : | : | : | 340 | 307 AKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTK 340
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                        FILING DATE: 29-JUN-1990
APPLICATION NUMBER: US 07/457,196
                                                                          FILING DATE: 29-DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1989
APPLICATION NUMBER: US 07/546,114
                                                                                                                                                                              NAME: Ceerr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI 5190
TELECOMMUNICATION:
TELECOMMUNICATION: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear

MOLECULE TYPE: procein

SEQUENCE DESCRIPTION: SEQ ID NO: 104:
US-11-169-232-104
                                                                                                                                                                                                                                                                                         TELEPHONE: (617)876-1170
TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 104:
                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1140 amino acids
                                                                                                                                                       ATTORNEY/AGENT INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 1363;
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Best Local Similarity 20.1%; Pred. No. 21;
Matches 55; Conservative 35; Mismatches 111; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  196 RHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHK----
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                                                                                                                                              FILING DATE: 16. Apr. 2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18. ADV. 1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29. JUN-1990
APPLICATION NUMBER: US 07/57,196
FILING DATE: 29. DEC-1989
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08. AUG-1989
ATTORNEY, AGENT THORNATION:
                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/124,557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 52:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: CBGIT, LUADIN
REGISTRATION UNDMEER: 31,822
REFERENCE/DOCKET UNDMEER: GI 51
TELECOMMUNICATION INFORMATION:
TELEPHONE: (G17)876-1170
TELEPAK: (G17)876-1170
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
FILING DATE: 28-Jun-2005
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1363 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
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US-11-169-232-2
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83 KKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQI--VHYIMKNEANADVLKAM-VA 139
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COMPUTER: ITEM PC COMPATION
COMPUTER: IBM PC COMPATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/169,232
FILING DATE: 38-Jun-2005
CLASSIFICATION: «UNKNOWN»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHKRWHPIKPTNKSRESRPRROGEVTVLSVGRFRVTKVEHK-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 5.8%; Score 82.5; DB 7; Best Local Similarity 20.1%; Pred. No. 22; Matches 55; Conservative 35; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 AKETQSIEKTSAKDLAPTSKVLAKPTPKAETTTK 340
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                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/124,557
FILING DATE: 16-Apr-2002
APPLICATION NUMBER: US 07/643,502
FILING DATE: 18-JAN-1991
APPLICATION NUMBER: US 07/546,114
FILING DATE: 29-JUN-1990)
APPLICATION NUMBER: US 07/457,196
FILING DATE: 29-DEC-1899
APPLICATION NUMBER: US 07/390,901
FILING DATE: 08-AUG-1899
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Job time : 19 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TOPOLOGY: linear; SEQUENCE TYPE: protein; SEQUENCE DESCRIPTION: SEQ ID NO: 2: US-11-169-232-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Cserr, Luann
REGISTRATION NUMBER: 31,822
REFERENCE/DOCKET NUMBER: GI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (617)876-1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (617)876-5851
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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241 ERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
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US-10-620-562-2
; Sequence 2, Application US/10620562
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522, App
4, Appli
515, App
680, App
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                                                                                                                 February 23, 2006, 12:08:48; Search time 163 Seconds (without alignments) 694.673 Million cell updates/sec
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1 MAPRALPGSAVLAAAVFVGG......ETVNGEVPATPVKRERSGTE
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US108_PUBCOMB.pep:*
                GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-10-620-562-2

US-09-933-762-294

US-10-004-860-294

US-10-023-288-294

US-09-913-767-633

US-10-023-282-63

US-10-004-860-633

US-10-004-860-633

US-10-005-562-6

US-09-057-951-4

US-09-057-951-2

US-09-057-951-2

US-09-057-951-2

US-09-1112-2

US-09-1112-2

US-09-1112-2

US-10-105-150-2

US-10-105-150-4

US-10-105-150-4

US-10-105-150-4

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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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Maximum DB
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Sequence 634, App
Sequence 734, App
Sequence 1534, Ap
Sequence 168, Ap
Sequence 2688, Ap
Sequence 10933, A
Sequence 17, Appl
Sequence 17, Appl
Sequence 6, Appli
Sequence 8, Appli
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Fatent No. US20020098163A1
GENERAL INFORMATION:
APPLICANT' Zeng et al.
TITLE OF INVERTION:
FILE REFERENCE: PF530
CURRENT APPLICANTION NUMBER: US/09/910,562
CURRENT APPLICANTION NUMBER: 60/221,143
FRIOR FILING DATE: 2000-07-23
FRIOR FILING DATE: 2000-07-24
FRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE PARENT PAR
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100.0%; Score 1426; DB 3;
Best Local Similarity 100.0%; Pred. No. 4.4e-118;
Matches 271; Conservative 0; Mismatches 0;
US-09-933-767-634
US-10-004-860-634
US-10-0023-282-634
US-10-620-562-7
US-09-796-692-1534
US-10-010-862-1534
US-10-010-862-1534
US-10-154-8848-1534
US-10-154-8848-1534
US-10-164-324-1534
US-10-164-324-1534
US-10-437-963-19214
US-10-437-963-19093
US-10-369-493-19093
US-10-290-631-6
US-10-290-631-8
US-10-290-631-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; ORGANISM: homo sapiens
US-09-910-562-2
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PRIOR
PRIOR
                                                            ## APPLICANT: Zeng, Z et al.

## APPLICANT: Zeng, Z et al.

## TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22

## TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22

## TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22

## CURRENT APPLICATION NUMBER: US/10/620,562

## PRIOR PELICATION NUMBER: US/210/143

## PRIOR PILING DATE: 2000-07-23

## PRIOR PELING DATE: 2000-07-24

## PRIOR PILING DATE: 2000-07-24

## PRIOR PILING DATE: 2000-07-24

## NUMBER OF SEQ ID NOS: 10

## SEQ
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P2
CURRENT APPLICATION NUMBER: US/09/933,767
CURRENT PILING DATE: 2001-08-22
FRICH APPLICATION NUMBER: PCT/US01/05614
FRICH PRICH APPLICATION NUMBER: 60/184,836
FRICH FILING DATE: 2000-02-3
FRICH FILING DATE: 2000-03-29
FRICH FILING DATE: 2000-03-29
FRICH FILING DATE: 1998-12-04
FRICH FILING DATE: 1998-12-04
FRICH FILING DATE: 1998-06-04
FRICH FILING DATE: 1998-06-04
FRICH FILING DATE: 1999-06-06
FRICH APPLICATION NUMBER: 60/048,885
FRICH APPLICATION NUMBER: 60/049,375
FRICH FILING DATE: 1997-06-06
FRICH APPLICATION NUMBER: 60/048,881
FRICH FILING DATE: 1997-06-06
FRICH APPLICATION NUMBER: 60/048,881
FRICH FILING DATE: 1997-06-06
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Publication No. US20050090436A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: PRT
ORGANISM: homo sapiens
                                         GENERAL INFORMATION
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US-09-933-767-294
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R APPLICATION NUMBER: 60/049,020
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,876
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,895
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PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,896
PILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,019
BILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,970
                                                                                                                                                                                                                                                                                                                                                                                                           PILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,882
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,899
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APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048, 901
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,373
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APPLICATION WUMBER: 60/048,917
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,949
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,897
FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/070,923
FILING DATE: 1997-12-18
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APPLICATION NUMBER: 60/048,972
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APPLICATION NUMBER: 60/048,894
                                                                                                                                                                                                                                                                                                          FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,971
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APPLICATION NUMBER: 60/048,964
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,962
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APPLICATION NUMBER: 60/068,054
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LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PEATURE:
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: 207 Human Secreted Proteins
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US-10-004-860-294
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CURRENT APPLICATION NUMBER: US/10/023,282

CURRENT FILING DATE: 2001-12-20

EARLIER APPLICATION NUMBER: 09/205,258

EARLIER APPLICATION NUMBER: 09/205,258

EARLIER APPLICATION NUMBER: PCT/US98/11422

EARLIER APPLICATION NUMBER: 60/048,885

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,375

EARLIER APPLICATION NUMBER: 60/049,881

EARLIER APPLICATION NUMBER: 60/048,881

EARLIER PILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,896

EARLIER PILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-
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APPLICATION NUMBER: 60/048,971
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,964
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Publication No. US20030092893A1
                             ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: SITE
LOCATION: (82)
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LOCATION: (80)
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LOCATION: (103
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KBY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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; Publication No. US20030065160A1
; GENERAL INFORMATION:
; APPLICANT: YOUNG et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REPERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT PILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 2001-12-07
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PATENTIN Ver. 2.0
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.; OTHER INFORMATION: Xaa equals stop translation US-09-33-767-294
PRIOR APPLICATION NUMBER: 60/073,160
PRIOR FILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-07-15
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Best Local Similarity 95.0%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: PRT
ORGANISM: Homo sapiens
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US-10-004-860-294
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LENGTH: 103
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LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                         Query Match 33.5%; Score 477.5; DB 4; Length 103; Best Local Similarity 95.0%; Pred. No. 2e-34; Matches 96; Conservative 0; Mismatches 4; Indels 1
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NAME/KEY: STTE

LOCATION: (103)

COTATION: (203)

STEP

LOCATION: (203)

STEP

LOCATION: (203)

HOSMWATION: Xaa equals stop translation
US-10-023-282-294
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                  FEATURE:
NAME/KEY: SITE
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US-09-933-767-633
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids PEATURE:
NAME/KEY: SITE
LOCATION: (80)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (81)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
EARLIER PILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,882

EARLIER PILING DATE: 1997-06-06

EARLIER PILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,903

EARLIER PILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,97

EARLIER PILING DATE: 1997-06-06

EARLIER APPLICATION NUMBER: 60/048,97

EARLIER APPLICAT
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ORGANISM: Homo sapiens
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sequence 6, Application US/09910562
sequence 7 TTLE OF INVENTION: Human Tumor Necrosis Factor Receptors TR21 and TR22
still REFERENCE: PF530
current Application NUMBER: US/09/910,562
current Filling Date: 2001-07-27
sprior Application NUMBER: 60/221,143
prior Application NUMBER: 60/220,116
prior Application NUMBER: 60/220,116
sprior Filling Date: 2000-07-27
sprior Filling Date: 2000-07-24
sumber OF SEQ ID NOS: 10
sportware: Patentin version 3.0
sportware: Patentin version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97 EEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG 156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (56)..(57)
OTHER INFORMATION: Xaa equals any amino acid
NAME/KEY: SITE
LOCATION: (60)..(60)
OTHER INFORMATION: Xaa equals any amino acid
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LOCATION: (83)..(84)
OTHER INFORMATION: Xaa equals any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 SPPVSPGPLSPGGTPG 172
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us-10-620-562-2.rapbm

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PRINCE TITLE OF INVESTION 207 Human Secreted Proteins PRIOR APPLICATION NUMBER: 2001-08-22 Human Secreted Proteins PRIOR APPLICATION NUMBER: 60/193,170 Human Secreted PRIOR APPLICATION NUMBER: 60/193,170 Human Selected PRIOR APPLICATION NUMBER: 60/193,170 Human Selected PRIOR PRIOR PLING DATE: 2000-02-21 Human Secreted PRIOR PLING DATE: 2000-02-21 Human Secreted PRIOR PLING DATE: 1991-06-06 Human Secreted PRIOR PLING DATE: 1991-06-06 Human Secreted PRIOR PLING DATE: 1997-06-06 Human Secreted PRIOR PLING DATE: 1997-06-06 Human Secreted PRIOR APPLICATION NUMBER: 60/048, 885 Human Secreted PRIOR PLING DATE: 1997-06-06 Human Secreted PRIOR APPLICATION NUMBER: 60/048, 999 Human Secreted PRIOR PLING DATE: 1997-06-06 Human Secreted PROTECATION NUMBER: 60/048, 915 Human Secreted PRIOR PLING DATE: 1997-06-06 Human Secreted PROTECATION NUMBER: 60/048, 915 Human Secreted PROTECATION NU
Sequence 633, Application US/09933767
Publication No. US20030181692A1
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/048,949
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LOCATION: (56)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE LOCATION: (57)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE LOCATION: (60) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (84) OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids ; LOCATION: (165) ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-933-767-633 PRIOR PILING DATE: 1997-06-06
PRIOR APPLICATION NUMBER: 60/048,883
PRIOR PILING DATE: 1997-06-06
PRIOR PRILING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PELING DATE: 1997-06-06
PRIOR PILING DATE: 1997-12-18
PRIOR PELING DATE: 1997-12-18
PRIOR PILING DATE: 1997-06-06
PRIOR PILING DATE: 1997-03-01-30
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-05-18 PLICATION NUMBER: 60/048,974 LING DATE: 1997-06-06 TYPE: PRT ORGANISM: Homo sapiens NAME/KEY: SITE NAME/KEY: SITE

Query Match

23.3%; Score 332; DB 3; Length 181

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207 Human Secreted Proteins
     APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteir FILE REPERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/10/023,282
CURRENT FILING DATE: 2001-12-20
EARLIER APPLICATION NUMBER: 09/205,258
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER PILING DATE: 1998-06-04
EARLIER FILING DATE: 1998-06-06
EARLIER APPLICATION NUMBER: 60/049,375
EARLIER FILING DATE: 1997-06-06
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ER APPLICATION NUMBER: 60/048, 901

ER PILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048, 915

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/049, 019

ER FILING DATE: 1997-06-06

ER PELING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER PILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048, 972

ER FILING DATE: 1997-06-06

ER APPLICATION NUMBER: 60/048, 972

ER PILING DATE: 1997-06-06
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R APPLICATION NUMBER: 60/048,876
R PILING DATE: 1997-06-06
R RILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,895
R APPLICATION NUMBER: 60/048,894
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R RILING DATE: 1997-06-06
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EX FILING DATE: 1997-06-06
EX APPLICATION NUMBER: 60/048, 949
EX APPLICATION NUMBER: 60/048, 974
EX PILING DATE: 1997-06-06
EX APPLICATION NUMBER: 60/048, 883
EX PLING DATE: 1997-06-06
EX APPLICATION NUMBER: 60/048, 897
EX ELING DATE: 1997-06-06
EX APPLICATION NUMBER: 60/048, 897
EX ELING DATE: 1997-06-06
EX APPLICATION NUMBER: 60/048, 898
EX ELING DATE: 1997-06-06
EX EXPELICATION NUMBER: 60/048, 898
EX ELING DATE: 1997-06-06
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R APPLICATION NUMBER: 60/048,899

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R FILING DATE: 1997-06-06

R APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/048,881
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,880
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FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,882
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APPLICATION NUMBER: 60/048,875
FILING DATE: 1997-06-06
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APPLICATION WUMBER: 60/048,896
ELING DATE: 1997-06-06
APPLICATION WUMBER: 60/049,020
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FILING DATE: 1997-06-06
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                                                                                                                                             NAME/KEY: SITE
LOCATION: (56)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
LOCATION: (57)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-004-860-633
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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     Pred. No. 3.6e-21;
3; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: P2007P1
CURRENT APPLICATION NUMBER: US/10/004,860
CURRENT FILING DATE: 2001-12-07
Prior Application removed - See File Wrapper or Palm NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 633
LENGTH: 181
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8-10-004-860-633
Sequence 633, Application US/10004860
Publication No. US20030065160A1
GENERAL INFORMATION:
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US-10-023-282-633
Sequence 633, Application US/10023282
; Publication No. US20030092893A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         157 SPPVSPGPLSPGGTPG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 SPPVSPGLCHQGGRQG 151
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          85.5%;
Best Local Similarity 85.59
Matches 65; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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LOCATION: (60)
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OTHER INFO
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PEATURE:

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NS-09-05-951-4

Sequence 4, Application US/09057951

Sequence 4, Application US/09057951

Patent No. US20020025551A1

GENERAL INFORMATION:

APPLICANT: Holtzman, Douglas

TITLE OF INVENTION: PROTEIN FAMILY AND USES THEREOF

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSER: Fish & Richardson P.C.

STREET: 225 Franklin Street

COLTY: BOSCON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTY 1 USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: Diskette

COMPUTER: Diskette

COMPUTER: Diskette

CORRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/057,951

APPLICATION NUMBER: US/09/057,951

APPLICATION NUMBER: US/09/057,951

ATTORNEY/AGENT INPORMATION:

NAME: Melklejohn, Ph.D., Anita L.

REGISTRATION NUMBER: 35,283

REFERENCE/POCKET NUMBER: 09404/046001

TELECOMMUNICATION INPORMATION:

TELECOMMUNICATION STORMATION:

TELEFRONE: 617/542-5070

TELEFRONE: 617/542-5070

TELEFRONE: 200154

INPORMATION POR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
          PRIOR APPLICATION NUMBER: 60/220,116
PRIOR FILING DATE: 2000-07-24
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              157 SPPVSPGPLSPGGTPG 172
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                                                                                                                                                                TYPE: PRT
ORGANISM: homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (56)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (165)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-023-282-633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16 KCCCVEKXXLINDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (84)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22
FILE REPERENCE: PF530C1
CURRENT APPLICATION NUMBER: US/10/620,562
CURRENT FILING DATE: 2003-07-17
PRIOR PLILOR DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2001-07-23
PRIOR FILING DATE: 2000-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 23.3%; Score 332; DB 4; Length 181; Best Local Similarity 85.5%; Pred. No. 3.6e-21; Matches 65; Conservative 3; Mismatches 8; Indels
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER FILING DATE: 1997-06-06
EARLIER PEDLICATION NUMBER: 60/048,963
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,878
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-02-06
EARLIER APPLICATION NUMBER: 60/092,921
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 1227
NUMBER OF SEQ ID NOS: 1227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SPPVSPGPLSPGGTPG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 SPPVSPCLCHQGGRQG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY: SITE
LOCATION: (56)
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NAME/KEY: SITE
LOCATION: (57)
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NAME/KEY: SITE
LOCATION: (60)
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NAME/KEY: SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO 633
LENGTH: 181
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97 EEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG
                                                                                                                                                                                                                                                                                                                                                                                                            0; Gaps
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                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (60)..(60)
OTHER INFORMATION: X equals any amino acid
PEATURE:
NAME/KEX: misc_feature
LOCATION: (56)..(57)
OTHER INFORMATION: X equals any amino acid
                                                                                                                                                                                                  LOCATION: (83)...(84)
OTHER INFORMATION: X equals any amino acid
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------ANEDTIGVLVRLITEKKENAAALEELLKE 225
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                                                                                                                                                                                                                                                                                                                                                226 ---YHSKQLVQTS---HRPVSKLPPAPPNVP--HICPHRHHLHTVQGLASLSGPCCSRCS 277
                                                                                                                                                                                                                                                                                                                                                                                                              |:| : ||||||||| :: 278 QKKWPEVLLSPEAVAATTPVPSLLPNPTRVPKAGAKAGRQGEITILSVGRFRVARI---- 333
                                                                                                                                                       TRQPGNGTRAGGPEETAAQYAVIAIVPVFCLMGLLGILVCNLLKRKGYHCTAHKEVGPGP 181
                                                                                                                                                                                                                                                                                                                                                                                          197 HKRWHFI--------KPTNKSRE-SRPRRQGEVTVLSVGRFRVTKVEHKS 237
                                                                                                                                 44 TPSPSNDTGNGHPE----YIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAE----
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82;
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                                              Length 408;
                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                         :69
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21.5%; Score 307; DB 3;
Best Local Similarity 31.0%; Pred. No. 1.9e-18;
Matches 84; Conservative 36; Mismatches 69,
                                            21.5%; Score 307; DB 4; 31.0%; Pred. No. 1.8e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: Window895
SOFTWARE: FASELEGO for Window8 Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/057,951
FILING DATE: 09-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Meik-lejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/046001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        334 --PEQRISSMVSEVKIITEAGPSWGDLPDSP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 NOKERRSIMSVSGAETVN-----GEVPATP 262
                                                                                      36; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: NOVEL MOLECULES OF THI
TITLE OF INVENTION: PROTEIN FAMILY AND USI
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09057951
Patent No. US20020025551A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible OPERATING SYSTEM: Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 430 amino acids
TYPE: amino acid
                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX; 200154
INFORMATION FOR SEQ ID NO:
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internal
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                Best Local Similarity
Matches 84; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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FRAGMENT TYPE:
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    US-10-105-150-4
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                                              Query Match
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                                                                                                                                                                                                                                                                                                                              182 GGGGSGINPAYRTED------ANEDTIGVLVRLITEKKENAALEELLKE 225
                                                                                                                                                                                                                                                                                                                                                                                    141 NSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVC--GHHLHTVGGV--VERDVCHRCR 196
                                                                                                                                                                                                                                                                                                                                                                                                                 226 ---YHSKQLVQTS---HRPVSKLPPAPPNVP--HICPHRHHLHTVQCLASLSGPCCSRCS 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KPTNKSRE-SRPRRQGEVTVLSVGRFRVTKVEHKS 237
                                                                                                                                                                                                               44 TPSPSNDTGNGHPE----YIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAE----
                                                                                                                                                                           Gaps
                                                                                                                                                                         82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 4, Application US/10105150
Publication No. US20020119524A1
GENERAL INFORMATION:
APPLICANT: Holtzman, Douglas
TITLE OF INVENTION: NOVEL MOLECULES OF THE T129-RELATED
                                                                                                                            ; Score 307; DB 3; Length 408;
; Pred. No. 1.8e-18;
36; Mismatches 69; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible
COMPUTER: FARTING SYSTEM: Windows95
SOFTWARE: PARESEG for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/105,150
FILING DATE: 25-MAR-2002
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/057,951
FILING DATE: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 09404/046001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             238 NQKERRSLMSVSGAETVN-----GEVPATP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |:|: |: |: |: |334 --PEQRISSMVSEVKTITEAGPSWGDLPDSP 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: 1918 & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 408 amino acida
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                          Query Match
Best Local Similarity 31.0%;
Matches 84; Conservative 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4:
408 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 HKRWHFI-----
                 TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-057-951-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEX: 200154
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US-10-105-150-4
LENGTH:
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204 GGGGSGINPAYRTED------ANEDTIGVLVRLITEKKENAALEELLKE 247
                                                                                                                              141 NSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVC--CHILHTVGGV--VERDVCHRCR 196
                                                                                                                                                   248 ---YHSKQLVQTS---HRPVSKLPPAPPNVP--HICPHRHILHTVQGLASLSGPCCSRCS 299
                                                                                                                                                                                                                        |:| |: |||||||| :: |||| :: ||||| :: 300 QKKMPEVLLSPEAVAATTPVPSLLDNPTRVPKAGAKAGRQGEITILSVGRPRVARI---- 355
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                                                     ------QDIEEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVAD 140
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                                                                                                                                                                                                                                                                                                   --PEQRISSMVSEVKTITEAGPSWGDLPDSP 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Ni, Jian
APPLICANT: Ruben, Steven M.
TITLE OF INVENTION: TUPE Related Gene 12
FILE REFERENCE: PP490P1
CURRENT APPLICATION NUMBER: US/09/836,607
CURRENT FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/198,388
PRIOR FILING DATE: 2000-04-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1999-10-19
PRIOR FILING DATE: 1998-10-20
PRIOR FILING DATE: 1998-10-20
SOFTWARE: PATENTIN OWER: 60/104,950
FRIOR FILING DATE: 1998-10-20
SOFTWARE: PATENTIN OF: 30-7
                                                                                                                                                                                                                                                                              238 NOKERRSLMSVSGAETVN-----GEVPATP
                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 2, Application US/09836607; Patent No. US20020098541A1; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
US-09-836-607-2
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RESULT 15 US-09-421-112-2 ; Sequence 2, Application US/09421112

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Best Local Similarity 31.0%; Pred: No. 1.9e-18; Matches 84; Conservative 36; Mismatches 69,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              238 NOKERRSIMSVSGAETVN-----GEVPATP 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --PEQRISSMVSEVKTITEAGPSWGDLPDSP 384
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: NI, Jian
TITLE OF INVENTION: TAVEN M.
TITLE OF INVENTION: TWER Related Gene 12
FILE REFERENCE: PF490
CURRENT APPLICATION NUMBER: US/09/421,112
CURRENT FILING DATE: 1999-10-19
EARLIER APPLICATION NUMBER: 60/104,950
RARLIER PILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PATENTING Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: February 23, 2006, 12:12:15
Job time : 164 secs
                                                                                                                                                                                                                                                                                                                                                LENGTH: 430
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-421-112-2
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R APPLICATION NUMBER: 60/049,375
RR FILING DATE: 1997-06-06
RR PILING DATE: 1997-06-06
RR RPILING DATE: 1997-06-06
RR PILING DATE: 1997-06-06
RR PILING DATE: 1997-06-06
RR PILING DATE: 1997-06-06
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2688, Ap
2688, Ap
8, Appli
6, Appli
13, Appli
3, Appli
14242, A
                                                                                                                                   February 23, 2006, 12:08:03; Search time 47 Seconds (without alignments) 476.704 Million cell updates/sec
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Sequence
Sequence
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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l: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
l: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
l: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
l: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
l: /cgn2_6/ptodata/1/iaa/PGTUS_COMB.pep:*
l: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
l: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
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US-10-004-866-294
US-01-004-866-233
US-10-004-866-633
US-10-004-866-633
US-09-949-016-10986
US-09-205-258-634
US-10-004-866-634
US-09-248-796A-15758
US-09-248-796A-15758
US-09-985-950-6
US-08-985-950-6
US-09-546-049-6
US-09-915-915-316
US-09-310-918-216
US-09-310-918-311
US-09-310-918-311
                                                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                        572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                           OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match
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Perfect score:
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Maximum DB seq
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No.
                                                                                                                                           Run
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APPLICATION NUMBER: 60/048,885 FILING DATE: 1997-06-06

DATE: 1998-06-04

R APPLICATION NUMBER: 60/048,899
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,893
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06
R FILING DATE: 1997-06-06

APPLICATION NUMBER: 60/048,892 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,915 FILING DATE: 1997-06-06

Sequence

Sequence Sequence

FILING DATE: 1997-06-06

28	87.5	6.1	559	0	US-08-781-986A-5251	Segnence 52	5251, Ap
29	87.5	6.1	1420	-	US-08-540-804-14		Appl
30	87.5	6.1	1420	н	US-08-218-265-14		
31	87.5	6.1	1420	7	US-08-521-872-14		
32	87.5	6.1	1420	~	US-08-590-399-14		Appl
33	87.5	6.1	1420	~	US-09-487-558B-356		'n
34	87	6.1	191	~	US-09-198-452A-335		
35	87	6.1	902	~	US-09-438-185A-319		319, App
36	86.5	6.1	290	~	US-09-270-767-35246		
37	86.5	6.1	290	~	US-09-270-767-50463		_
38	98	6.0	204	~	US-08-529-055-51		Appl.
39	98	6.0	547	~	US-09-221-013A-14		
40	98	6.0	729	7	US-09-949-016-11190		
41	98	9	2753	~	US-09-949-016-7659		.59. Ap
42	98	9.0	2753	~	US-09-949-016-7660		7660. Ap
43	98	6.0	3924	~	US-09-538-092-1246		46. AD
44	85.5	9	168	~	US-08-529-055-55		S. Appl
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TIS-09-20	KESULT 1 TIS-09-205-258-294	24					
Seguer	ace 294.	Applica	ation U	8/0	9205258		
; Patent	Patent No. 6525174	5174					
, GENER	GENERAL INFORMATION:	ATION:					
, APPL	APPLICANT: Young et	oung et	al.				
; TITL	TITLE OF INVENTION:	ENTION:	207 Hur	man	207 Human Secreted Proteins		
, FILE	FILE REFERENCE: PZ007P1	E: PZ0	07P1				
; CURRI	ENT APPLI	CATION	NUMBER	ă 	CURRENT APPLICATION NUMBER: US/09/205,258		
, CURRENT	ENT PILIN	IG DATE	FILING DATE: 1998-12-04	12-(24		
; EARL	IER APPLI	CATION	NUMBER	<u>م</u>	EARLIER APPLICATION NUMBER: PCT/US98/11422		

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LOCATION: (78)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (80)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: SITE LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
            1 MAPRALPGSAVLAAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA 60
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                                                                                                        61 YALVPVFFIMGLFGVLIC-HLLKKKGYRCTTEAEQDIEEEK 100
                                                                                                                                          61 YALVPVFFIMGLFGVLIXPXXXKKKGYRCTTEAEQDIEEEK 101
                                                                                                                                                                                                                                                                                             Sequence 294, Application US/10004860

Patent No. 6914047

GENERAL INFORMATION:

APPLICANT: VOUNG et al.

TITLE OF INVENTION: 207 Human Secreted Proteins

TITLE OF INVENTION: 207 Human Secreted Proteins

TITLE PEPLICATION NUMBER: US/10/004,860

CURRENT FILING DATE: 2001-12-07

Prior Application removed - See File Wrapper or Palm

NUMBER OF SEQ ID NOS: 1227

SOFTWARE: Patentin Ver. 2.0

SEC ID NO. 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 YALVPVFFIMGLFGVLIC-HLLKKKGYRCTTEAEQDIEEEK 100
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95.0%; Pred. No. 1.3e-40;
tive 0; Mismatches 4;
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| Patent No. 6525174
| GENERAL INFORMATION:
| APPLICANT: Young et al. |
| TILLE OF INVENTION: 207 Human Secreted Proteins |
| FILE REFERENCE: PEO07P1 |
| CURRENT APPLICATION NUMBER: US/09/205,258 |
| CURRENT FILING DATE: 1998-12-04 |
| EARLIER FILING DATE: 1998-06-04 |
| EARLIER FILING DATE: 1998-06-04 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Xaa equals stop translation
US-10-004-860-294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: SITE
LOCATION: (81)
OTHER INFORMATION: Xaa equals any
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Best Local Similarity 95.0
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: SITE
                                                                                                                                                                                                                                                                                    US-10-004-860-294
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LOCATION: (80)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
LOCATION: (82)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 1.3e-40;
0; Mismatches 4; Indels 1;
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EARLIER APPLICATION NUMBER: 60/049,019
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,972
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER APPLICATION NUMBER: 60/048,916
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER APPLICATION NUMBER: 60/048,917
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 199
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Best Local Similarity 95.0%;
Matches 96; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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LOCATION: (81)
OTHER INFORMATION:
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LOCATION: (103)
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,972
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,916
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,373
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,374
R PILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/049,979
R APPLICATION NUMBER: 60/049,979
R PILING DATE: 1997-06-06
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PELLING DATE: 1997-06-06

PILING DATE: 1997-06-06

APPLICATION NUMBER: 60/048,915

FILING DATE: 1997-06-06

FILING DATE: 1997-06-06

APPLICATION NUMBER: 60/049,019

FILING DATE: 1997-06-06
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R APPLICATION NUMBER: 60/048,897
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,898
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/048,992
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APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,901
                                                                                                         FILING DATE: 1997-06-06
APPLICATION WUMBER: 60/048,880
ELING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,896
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APPLICATION NUMBER: 60/049,876
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,895
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FILING DATE: 1997-06-06
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,894
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APPLICATION NUMBER: 60/048,971
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,964
  FILING DATE: 1997-06-06
APPLICATION WUMBER: 60/049,375
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,881
                                                                                                                                                                                                          FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/049,020
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PPLICATION NUMBER: 60/048,882
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APPLICATION NUMBER: 60/048,899
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APPLICATION NUMBER: 60/048,883
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PPLICATION NUMBER: 60/048,963
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APPLICATION NUMBER: 60/048,877
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APPLICATION NUMBER: 60/048,974
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LOCATION: (56)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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NAME/KEY: SITE
LOCATION: (57)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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LOCATION: (60)
OTHER INFORMATION: Xaa equala any of the naturally occurring L-amino acids
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NAMB/KEY: SITE
LOCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; LOCATION: (165); OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-205-258-633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     76 KKKKVEKXXLINDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPG 135
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OTHER INFORMATION: Xea equals any of the naturally occurring L-amino acids PRATURE:
NAME/KEY: SITE
LOCATION: (57)
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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; Patent No. 6914047
; GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/10/004,860
; CURRENT FILING DATE: 2001-12-07
; Prior Application removed - See File Wrapper or Palm
; NUMBER F SEQ ID NOS: 1227
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 633
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER PILING DATE: 1998-07-15
; EARLIER PILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SGFTWARE: Patentin Ver. 2.0
; SEQ ID NO 633
; LENGTH: 181
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136 SPPVSPGLCHQGGRQG 151
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
PEATURE:
NAME/KEY: SITE
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NAME/KEY: SITE
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NAME/KEY: SITE
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NAME/KEY: SITE
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234 EHKSNOKERRSLMSV----SGAETVNGEVPATPVKR 265
                                                   427 EKRYGLHEHRDGSPTDRSWGSGVSTTGSREYVSPADK 463
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TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
                                                                                                                                                                                                                                                                                                                                              CURRENT FILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/111422
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EARLIER APPLICATION NUMBER: 60/048,885
EARLIER FILING DATE: 1997-06-06
EARLIER PLING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/049,891
EARLIER APPLICATION NUMBER: 60/048,891
EARLIER FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,893
FILING DATE: 1997-06-06
APPLICATION NUMBER: 60/048,900
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APPLICATION NUMBER: 60/048,949
FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/048,964
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FILING DATE: 1997-06-06
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APPLICATION NUMBER: 60/049,373
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Patent No. 6525174
GENERAL INFORMATION:
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: SITE
COCATION: (83)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
PEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----HTVHLGSAAPCLHCSRSKRPPLVRQGRSKEGKSRP-RTGETTVFSVGRFRVTHI 426
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                 Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          265 HGLYMLFLAULVFFLMGLVGFMICHVLKKKGYRCRTSRGSEPDDAQLQPPE-DDDMNE-- 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 DTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                322 DIVERIVECTIONEANAEALKEMIGDS---EGEGTVQLSS-----VDATSSLQDGAPSHH 373
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 VCGHHLHTVGGVVERDVCHRCRHKRWHFIKP-TNKSRESRPRRQGEVTVLSVGRFRVTKV 233
                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 332; DB 2;
Pred. No. 1.6e-25;
3; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 6/241,755
PRIOR APPLICATION NUMBER: 6/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-0-03
PRIOR PILING DATE: 2000-0-05
FRIOR PILING DATE: 2000-0-05
SPRIOR PILING DATE: 2000-0-06
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 10986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      157 SPPVSPGPLSPGGTPG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    136 SPPVSPGLCHQGGRQG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
23.3%;
Best Local Similarity 85.5%;
Matches 65; Conservative
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Best Local Similarity 36.99
Matches 80; Conservative
                                                                       LOCATION: (60)
OTHER INFORMATION:
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US-09-949-016-10986
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; ORGANISM: Human
US-09-949-016-10986
                                                                                                                                                                                                                                                NAME/KEY: SITE
LOCATION: (84)
                                                   NAME/KEY: SITE
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US-10-104-047-2688
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10.3%; Score 147; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.9e-08;
Matches 29; Conservative 0; Mismatches 0; Indels
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NUMBER OF SEQ ID NOS: 1227
SOFTWARE: Patentin Ver. 2.0
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Pred. No. 5.9e-08;
0; Mismatches 0;
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Batent No. 6914047

GENERAL INFORMATION:
APPLICANT: Young et al.
TITLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1

CURRENT APPLICATION NUMBER: US/10/004,860

CURRENT FILING DATE: 2001-12-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 IMKNEANADVLKAMVADNSLYDPESPVTP 152
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EARLIER APPLICATION NUMBER: 60/048,974
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,897
EARLIER APPLICATION NUMBER: 60/048,998
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER APPLICATION NUMBER: 60/048,962
EARLIER APPLICATION NUMBER: 60/048,963
EARLIER FILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER FILING DATE: 1998-07-18
EARLIER FILING DATE: 1998-07-30
NUMBER OF SEQ ID NOS: 1227
SEQ ID NO 634
EARLIER PATENT VET. 2.0
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100.0%; Pre
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; ORGANISM: Homo sapiens
US-09-205-258-634
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CORGANISM: Homo sapiens
US-10-004-860-634
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Best Local Similarity
Matches 29; Conservat
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US-09-248-796A-15758

Sequence 15758, Application US/09248796A

Patent No. 6747137

GENERAL INFORMATION:

APPLICANT: Keith Weinstock et al

RESULT 8

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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR PAPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
PRIOR FILING DATE: 1998-02-13
SEQ ID NOS: 28208
SEQ ID NO 15758
LENGTH: 819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60 AYALVPVFFIMGLFGVLICHLLKKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTV-G 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167 ÓIVASIOPPOSPPETPOSGPKACSVEELYAIPPDADVAKSTPKSTPVRPKSLFTSQPSGE 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .------DPE-SPVTPS-----TPGSPPVSPGPLSPGGTPGKHVKGHHLH 181
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                                                                                                                                                                                                                                                                                                                                                                                                                    Length 819;
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20.6%; Pred. No. 0.32;
tive 37; Mismatches 87; Indels 153
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TITLE OF INVENTION: NO. 6943241e1 full length cDNA
FILE REPERENCE: H1-A0105
CURRENT APPLICATION NUMBER: US/10/104,047
CURRENT PILING DATE: 2002-03-25
PRIOR APPLICATION NUMBER:
PRIOR PLILING DATE:
SOFTWARE: PRECED NOS: 4096
SOFTWARE: PRECED NOS: 4096
SOFTWARE: PRECED NOS: 4096
SOFTWARE: PRECED NOS: 4096
SEQ ID NO 2688
                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.3%; Score 103.5; DE Best Local Similarity 27.1%; Pred. No. 0.19; Matches 26; Conservative 21; Mismatches
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Patent No. 6943241
GENERAL INFORMATION:
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Beet Local Similarity 20.00,
The 72; Conservative
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; ORGANISM: Homo sapiens
US-10-104-047-2688
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126 GPDSPDTEPGSSAGPTQRPSDNSHNEHAPASQG-----LKAEHLYILIGVSVVFLFCLL 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89 TTEAEQDIEEEKVEKIELN---DSVNENSDTVGQIVHY-IMKNEANADVLKAMVADNSLY 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 SRTLHSRTETTPSPSNDTGNGHPEYIAYALVPV----FFIMGLFGVLICHLLKKKGYRC
                                                                                                                                                                                                                                                       APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes,
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.8%; Score 97; DB 2; Length 287; Best Local Similarity 22.7%; Pred. No. 0.19; Matches 58; Conservative 45; Mismatches 105; Indels
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SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/985,950
FILING DATE: US/08/985,950
CLASSIFICATION NUMBER: US/08/985,950
PILOR APPLICATION TO #15
PILOR APPLICATION NUMBER: US 60/041,279
PILOR APPLICATION NUMBER: US 60/041,279
PILOR APPLICATION NUMBER: US 60/033,181
PILING DATE: 16-DEC-1996
PROMER APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTONNEY/AGENT INPOMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTONNEY/AGENT INPOMBER: US 60/032,252
FILING DATE: US 60/032,252
                                                                                                                                                                                                                                                                                                                                                              E: DNAX Research Institute 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,090
REFERENCE / DOCKT NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
CMEDIUM TYPE: Floppy disk
CMEDTER: IBM PC compatible
OPERATING SYSTEM: PC_DOS/MS_DOS
                                                                                                                                                                               Sequence 8, Application US/08985950
Patent No. 6140076
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 287 amino acids TYPE: amino acids
       243 RSLMSVSGAETVNGEV 258
                                                     239 SALAAGSSQEVTYAQL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-985-950-8
                                                                                                                                                                                                                                                                                                                                                                                    STREET: 901 Califo
CITY: Palo Alto
STATE: California
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                                                                                                                                                          US-08-985-950-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 LLVLFCLH-RQNQIKQGPPRSKDEBQKPQQRPDLAVDVLERTADKATVNGLPEKDRETDT 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTEAEQDIEEEEKVEKIELN---DSVNENSDTVGQIVHY-IMKNEANADVLKAMVADNSLY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 GPDSPDTEPGSSAGPTQRPSDNSHNEHAPASQG-----LKAEHLYILIGVSVVFLFCLL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----CRHKRWHFIK---PTNKSRESRPRRQGEVTV----LSVGRFRVTKVEHKSNQKER 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPESPVT-PSTPGSPPVSP-----GPLSPGGTPGKHVCGHHLHTVGGV-VERDVCHR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16 AQTIHTQBEDLPRPSISAEPG-----TVIPLGSHVTFVCRGPVGVQTFRLERES--RS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34 SRTLHSRTETTPSPSNDTGNGHPEYIAYALVPV----FFIMGLFGVLICHLLKKKGYRC 88
                               224 SVGRFRVTKVE-HKSNQKERRSLMSVSGAETVNGEVPATPVKRERSGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 6.8%; Score 97; DB 2; Length 287; Best Local Similarity 22.7%; Pred. No. 0.19; Matches 58; Conservative 45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: R1094
COMPUTER READABLE FORM:
MEDIUM TYPE: R10949 disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 12-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
PRIOR APPLICATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELERPHONE: C60/082,29196
                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: DNAX Research Institute
STREET: 901 Callfornia Avenue
CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 287 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-985-950-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                  328
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126 GPDSPDTBPGSSAGPTQRPSDNSHNEHAPASQG-----LKAEHLYILIGVSVVFLFCLL 179
                                                                                                                     180 LLVLFCLH-RQNQIKQGPPRSKDEEQKPQQRPDLAVDVLBRTADKATVNGLPEKDRETDT 238
  --GPLSPGGTPGKHVCGHHLHTVGGV-VERDVCHR 194
                                                                                         195 ----CRHKRWHFIK---PTNKSRESRPRROGEVTV----LSVGRFRVTKVEHKSNQKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zurawski, Sandra M.
Zurawski, Gerard
Lanler, Lewis L.
Phillips Jr., Joseph H.
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48;
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PCC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,049
FILING DATE: 10-Apr-2000
PRIOR APPLICATION DATE: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/031,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 16-DEC-1996
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6.8%; Score 97; DB 2; Length 287; 22.7%; Pred. No. 0.19; Ve 45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: DX0670K TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                          Meyaard, Linde
Gorman, Daniel M.
McClanahan, Terrill K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Ching, Edwin P. REGISTRATION NUMBER: 34,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (650)852-9196
                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/09546049
Patent No. 6479638
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 287 amino acids
TYPE: amino acid
                                                                                                                                                                               243 RSLMSVSGAETVNGEV 258
                                                                                                                                                                                                                        239 SALAAGSSQEVTYAQL 254
    145 DPESPVT-PSTPGSPPVSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 6.8%;
Best Local Similarity 22.7%;
Matches 58; Conservative 4
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SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Palo Alto
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Adema,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                JS-09-546-049-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-546-049-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89 ITEAEQDIEEEKVEKIELN---DSVNENSDTVGQIVHY-IMKNEANADVLKAMVADNSLY 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 SRILHSRIETTPSPSNDTGNGHPEYIAYALVPV----FPIMGLFGVLICHLLKKKGYRC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AQTIHTQEEDLPRPSISAEPG-----TVIPLGSHVTFVCRGPVGVQTFRLERES--RS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48; Gaps
                                                                                                                                                                                                                                                                                                                                                Lanier, Lewis L.
Phillips Jr., Joseph H.
INVENTION: Isolated Mammalian Monocyte Cell Genes;
Related Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,049
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6.8%; Score 97; DB 2; Length 287; 22.7%; Pred. No. 0.19; tive 45; Mismatches 105; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION DAMER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-WARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: DX0670K
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSE: DNAX Research Institute
STREET: 901 California Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-546-049-6
                                                                                                                                                                                                               APPLICANT: Adema, Gosse Jan
Meyaard, Linde
Gorman, Daniel M.
McClanahan, Terrill K.
Zurawski, Sandra M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (650)852-9196
                                                                                                                                                   Sequence 6, Application US/09546049
Patent No. 6479638
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 287 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (650)496-1204
243 RSLMSVSGAETVNGEV 258
                           239 SALAAGSSQEVTYAQL 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 22.73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF
                                                                                                                                 09-546-049-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
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Best Local (
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-SRPRRQGE- 219
                                                     145 AVWVALSSLLVIVFIIIVLYMLRFKKYKQAGSHSNSFRLSNGRTEDVEPQSVPLLARSPS 204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 AYALVPVFFIMGLFGVLICHLLKKKGY------RCTTEAEQDIEEEKVEKIELNDS 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 VNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGG 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 EKNRYVNILPYDHSRVHLTPVEGVPDSDYINASFINGYQEKNKFIAAQGPKEETVNDFWR 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   202 FIKPINKS------SVGRFRVT 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91 AASTESGGTTISPNGSWLIENQFTDAITEPWEGNSSTAATTPETFP-PADET----PII
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AAAVFVGGAVSSP------LVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYI
                                                                                                             220 -VTVLSVGRFRVTKVEHKSNQKERRSLMSVSGAETVNGEVPATPVKRERS 268
                                                                                                                                        Query Match 6.6%; Score 94; DB 1; Length 793; Best Local Similarity 19.0%; Pred. No. 1.6; Matches 63; Conservative 51; Mismatches 124; Indels 94;
                                                                                                                                                                                                                                                                                                                                                                    NOVEL RECEPTOR-TYPE PHOSPHOTYROSINE PHOSPHATASE-ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 TPGKHV----CGH---HLHTVGGVVERDVCHRC-----RHKR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/015,985
FILING DATE: 10-FEB-1993
CLASSIPICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: PERNIE & EDMONDS
STREET: 1155 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
                          184 GGVVERDVCHRCRHKRWHFIKPTNKSRE
                                                                                                                                                                                                                                                     Sequence 3, Application US/08015985; Patent No. 5538886; GENERAL INFORMATION:
APPLICANT: Schlessinger, Joseph
TITLE OF INVENTION: NOVEL RECEPTOF
TITLE OF INVENTION: PHOSPHATASE-AL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (212) 790-9090
(212) 869-9741/8864
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Coruzzi, Laura A. REGISTRATION NUMBER: 30,742 REFERENCE/DOCKET NUMBER: 76 TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 793 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : 793 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-08-015-985-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
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US-08-015-985-3
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                                                                                                               ----CRHKRWHFIK---PTNKSRESRPRRQGEVTV----LSVGRFRVTKVEHKSNQKER 242
                                                                                                                                                                                                                                                                                  TTEAEQDIEEEKVEKIELN---DSVNENSDTVGQIVHY-IMKNEANADVLKAMVADNSLY 144
                                                                                                                                                                       DPESPVT-PSTPGSPPVSP-----GPLSPGGTPGKHVCGHHLHTVGGV-VERDVCHR 194
                                                                                                                                                                                                               126 GPDSPDTEPGSSAGPTQRPSDNSHNEHAPASQG----LKAEHLYILIGVSVVFLFCLL 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      137 MVADN--SLYDPESPVTPSTPGSPPVSPGPLSP-----GGTPGKHVCGHHLHTV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 590 AHEENPESILDEHVORVMRTPGCOSPGPGHRSPDSGHVAKTAVLGGTASGH--GKHVPKL 647
                                          16 AQTIHTQEEDLPRPSISAEPG-----TVIPLGSHVTFVCRGPVGVQTFRLERES--RS 66
34 SRILHSRIETIPSPSNDIGNGHPEYIAYALVPV----PFIMGLFGVLICHLLKKKGYRC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 6.7%; Score 95; DB 2; Length 992; Best Local Similarity 19.6%; Pred. No. 1.8; Matches 45; Conservative 35; Mismatches 94; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/890,865A
FILING DATE: 10-JUL-1997
CLASSIFICATION: 435
ATTONREY/AGENT INFORMATION:
NAME: White, John PRESENCE/DOCKET NUMBER: 0575/54249
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPRAK: (212)278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89 ITEAEQDIEEEKVEKIELNDSVNENSDTVGQIVHYIMKN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AXIN GENE AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/08890865A Patent No. 6307019 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Constantini, Franklin
APPLICANT: Zeng, Li
TITLE OF INVENTION: AXIN GENE ANI
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                              243 RSLMSVSGAETVNGEV 258
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 992 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
STATE: New York
COUNTRY: US
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US-08-890-865A-1
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us-10-620-562-2.rai

318 MIWEQNIATIUMVINLKERKECKCAQYWPDQGCWIYGNVRVSVEDVIVLVDYIVRKFSIQ 377 අ දු අ

Search completed: February 23, 2006, 12:09:26 Job time : 48 secs

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

February 23, 2006, 12:00:48; Search time 231 Seconds (without alignments) 827.698 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-10-620-562-2 1426 1 MAPRALPGSAVLAAAVFVGG......ETVNGEVPATPVKRERSGTE 271

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

2166443 segs, 705528306 residues Searched:

Total number of hits satisfying chosen parameters:

2166443

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database:

UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

																								1						
Description	homor.	•	OBK2)7 mus musculu	OBr385 mus musculu				Q4srn7 tetraodon n	Q9n092 macaca fasc	Q969z4 homo sapien	Q8bx43 mus musculu	Q8cft0 mus musculu	Q8brj3 mus musculu	Q6diw4 xenopus tro	Q5fvj4 rattus norv	Q68ev2 xenopus lae	Q6p4e7 homo sapien	Q6uxy2 homo sapien	Q8nc24 homo sapien	Q6nz11 brachydanio	Q4sel6 tetraodon n	Q48z05 tetraodon n	Q4w5d7 homo sapien	Q8i520 plasmodium	Q51rt1 magnaporthe	Q9i8g8 chelonia my	Q5fwn0 xenopus lae	Q5ah61 candida alb	Q5aip1 candida alb	Q4h3l1 ciona intes
SUMMAKLES		OBNEKT HOMAN	OBK217 MOUSE	OBR3S5 MOUSE	Q7TON2 XENLA	Q6NRQ3_XENLA	Q5M7X6_BRARE	Q4SRN7_TETNG	TR19L_MACFA	TR19L_HUMAN	TR19L_MOUSE	QBCFT0 MOUSE	Q8BRJ3_MOUSE	Q6DIW4_XENTR	Q5FVJ4_RAT	Q68EV2_XENLA	Q6P4E7_HUMAN	Q6UXY2_HUMAN	QBNC24_HUMAN	Q6NZ11_BRARE	Q4SEL6_TETNG	Q4SZ05_TETNG	Q4W5D7 HUMAN	Q81520_PLAF7	Q51RT1 MAGGR	Q918G8 CHEMY	Q5FWN0_XENLA	Q5AH61_CANAL	Q5AIP1_CANAL	Q4H3L1_CIOIN
DB	2	~ (N (N (N	~	~	N	~	-	-	-	7	7	~	~	~	N	~	~	~	~	~	~	~	~	~	~	~	N	N
% Query Match Length	271	271	707	143	223	224	280	281	430	430	436	294	303	325	302	327	303	303	303	401	163	25	29	2287	1244	392	875	800	800	515
& Query Match	100.0	9.66	69.	49.0	46.9	45.0	40.7	29.6	21.7	21.5	20.7	20.3	20.3	20.3	20.1	20.1	19.9	19.9	19.9	19.8	11.1	10.7	9.7	7.7	7.7	7.6	7.6	7.6	7.6	7.5
Score	1426	1421	966	669	699	641.5	581	422.5	309	307	295.5	289	289	289	286	286	284	284	284	282.5	158.5	152.5	138	110.5	110	109	109	108	108	107.5
Result No.		N C	n <	r 10	φ	7	6 0	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		26			53	30	31

Q55mf2 cryptococcu O6eugl oryza sativ	Q5k8c2 cryptococcu Q12075 pneumocysti		Oguéda plasmodium		Q728p6 leptospira Q8f2v5 leptospira	- '	Q5e9h4 bos taurus	Q7xe96 oryza sativ
Q55MF2_CRYNE O6EUQ1_ORYSA	QSK8C2_CRYNE Q12075_PNECA	Q52V19_9POTV Q26607_SCHMA	OSUGD4 PLABE	Q8V918_9POTV	Q728F6_LEPIC Q8F2V5_LEPIN	Q4S7I1_TETNG	Q5E9H4_BOVIN	Q7XE96_ORYSA
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805 795	805 1083	3140	1791	384	749	1279	751	1829
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106.5	105.5	105.5	104.5	103.5	103	103	102.5	102.5
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ALIGNMENTS

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Action No. 2011 St. 7. Feligold B.A., Grouse L.H., Derge J.G., Rausner R.D., Colling F.S., Wagner L.H., Derge J.G., Straubberg R.D., Colling F.S., Wagner L.H., Derge J.G., Struler G.D., Altschul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Blatch N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Halah F., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Bromatein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villaton D.K., Muzny D.W., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Radan A., Rodrigues S., Sanchez A., Muhting M., Madan A., Young A.C., Shevchenko Y., Bouffaxd G.G., Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C., Schmutz J., Myers R.M., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 NADILKAMYADNSVGDIESPVTPSTPGSPPVSPGPLSPGATPGKHVCGHHLHTVGGVVER 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                190 DVCHRCRHKRWHFIKPTNKSRESRPRRGGEVTVLSVGRFRVTKVEHKSNQKERRSLMSVS 249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        130 NADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVCGHHLHTVGGVVER 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MGLLGVLICHLLKKKGYRCTTBABQBVBBBKVBKIBLNDSINBNSDTVGQIVQYIMKNBA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IISSUE=Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQIVHYIMKNEA
                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
                                                                                                                                                                                                                                                                                                                           TISSUB=Embryo, and
Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.1%; Score 986; DB 2; Length 20
91.1%; Pred. No. 6.3e-67;
ive 9; Mismatches 9; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CS7BL/63; TISSUE=Embryo;
Director MGC Project;
Director MGC Project;
Submitted (PEB-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC031198; AAH66137.1; -; mRNA.
EMBL; BC066137; AAH66137.1; -; mRNA.
EMBL; BC066160; AAH66160.1; -; mRNA.
Ensembl; ENSWUSGO0000004781; Mus musculus.
MGI; MGI:2140767; AA536743.
SEQUENCE 202 AA; 22263 MW; 092F50EAF995E6B8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Strausberg R., submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
              01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
10-OKT-2005 (TrEMBLrel. 30, Last annotation update)
Expressed sequence AA536743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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                                                                                                                                                                                                                                                                           NUCLEOTIDE SEQUENCE.
STRAIN=FVB/N-3, and C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 69.1%;
Best Local Similarity 91.1%;
Matches 184; Conservative
                                                                                                                                                                                                        Muridae, Murinae, Mus
                                                                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE
                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-FVB/N-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
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셤
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                                                                                                                                                                                                        HTVGGVVERDVCHRCRHKRWHFIXPTNKSRESRPRRQGEVTVLSVGRPRVTKVEHKSNQK 240
                61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTFARQDIEEEKVEKIELNDSVNENSDTVGQI 120
                                                                                      VHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVCGHHL 180
                                                                                                            61 YALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEKIELNDSVNENSDTVGQI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 VHYIMKONEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVCGHHL 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2002 (TrEMBLrel. 22, Last annotation update)
CDNA PSEC0162 fis, clone PLACE1009772.
HOMO sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Signal Sequence and Keyword Trap in silico for Selection of Pull-Length Human cDNAs Encoding Secretion or Membrane Proteins from Oligo-Capped CDNA Libraries.";
DNA Res. 12:117-126(2005).
EMBL; AK075468; BAC11638.1; -; mRNA.
SEQUENCE 271 AA; 29310 MW; 385AAA0A97258FBD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRALHSRTETTPSPSNDTGNGHPEYIA
                                                                                                                                                                               HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAPRALPGSAVLAAAVFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSNDTGNGHPEYIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUB-Placenta,
Otsuki T., Ota T., Nishikawa T., Hayashi K., Suzuki Y., Yamamoto J.,
Otsuki T., Ota T., Nishikawa T., Hataon N., Kawai Y., Ishii S.,
Wakamatsu A., Kimura K., Sakamoto K., Hatano N., Kawai Y., Ishii S.,
Saito K., Kojima S., Sugiyama T., Ono T., Okano K., Yoshikawa Y.,
Aotsuka S., Sasaki N., Hattori A., Okumura K., Nagai K., Sugano S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.6%; Score 1421; DB 2; 99.6%; Pred. No. 7.7e-100; ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                   ,4 241 ERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                          271 AA
                                                                                                                                                                                                                                                                           ERRSLMSVSGAETVNGEVPATPVKRERSGTE 271
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                                                                                                                                                                                                                                                                                                                                                                                                                                     QBNBK1_HUMAN PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 270; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                           181
                                                                                                                                                                                                                                                                           241
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Q8K2J7 MOUSE
ID Q8K2J7_MC
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RESULT 2
QRNBLT 2
QRNBLT 1
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QEK2J7_MOUSE PRELIMINARY,

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   173 LKHNCKGHHLHTVGGVIEKDVCSRCSHKRWHHIKPAHKSKEHRRSRLGEVTVLSVGRFRV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 GHPEYIAYALVPVFFIMGLFGVLICHLLKKKKGYRCTTEAEQDIEEEKV-EKIELNDSVNE 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GKHVC-GHHLHTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRV 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPG-PLSPGGTP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAPRALPGSAVLA----AAVFVGGAVSSPLVAPDNGSSRTLHSR--TETTPSPSNDTGN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAPPAASGIPSIAPSLGPTAVWLGN.----RSDLGDVQALASRDLPTTTVTAGNNNKP 53
                                                                                                                                                                                                                                                                  OKFNames=RCJMB04 24124;
Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caldwell R.B., Kierzek A.M., Arakawa H., Bezzubov Y., Zaim J., Fiedler P., Kutter S., Blagodatski A., Kostovska D., Koter M., Plachy J., Carninci P., Hayashizaki Y., Buerstedde J.M.; Pull-length CDNAs from Chicken bursal lymphocytes to facilitate genefunction analysis."; Embl. 48.6K 6(2005).

EMBL; AJ851746; CA465380.1; -; mRNA.

Hypothetical protein.

SEQUENCE 288 AA; 31157 MW; 07DC2D83E938C7BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
59.9%; Score 854.5; DB 2; Length 288;
Best Local Similarity 61.0%; Pred. No. 9.3e-57;
Matches 177; Conservative 36; Mismatches 50; Indels 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TKVEHKSNOKERRSIMSVSGAETVNGEVPATPVKRE------RSGTE 271
                                                                                                                                                                                                            Last sequence update)
Last annotation update)
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Last sequence update)
Last annotation update)
                                                                                                                                               288 AA.
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                                                                                                                                                                                        Created)
                   PRT;
GAETVNGEVPATPVKRERSGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA536743 protein (Fragment).
Name=AA536743;
                                                                                                                                                                              10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30, Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, 01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                         QSF3A4 CHICK PRELIMINARY, QSF3A4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QBR3SS_MOUSE PRELIMINARY;
QBR3SS;
                                                                                                                                                                                                                                                                                                                                                                                                                  NUCLEOTIDE SEQUENCE.
STRAIN-CB; TISSUE-Bursa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9031;
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                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
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MEDLINE-238825; PubMed=12477932; DoI=10.1073/pnas.242603899;
MEDLINE-238825; PubMed=12477932; DoI=10.1073/pnas.242603899;
Strausberg R.L., Felingold E.A., Grouse L.H., Derge J.G.,
Altachul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Zeeberg B., Buetcw K.H., Schaefer C.F., Bhat N.K.,
Altachul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,
Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Altachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,
A. Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
A. McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Boask S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergen B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A. Raciquez A.C. Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield A.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield A.S.N., Krzywinski M.I., Marra M.A.;
Bud M.A., Schein J.E., Jones S.J.M., Marra M.A.;
Bud M.A., Schein J.E., Jones S.J.M., Marra M.A.;
Bud M.A., Schein J.E., Jones S.J.M., Marra M.A.;
Bud M.A., Schein J.E., Jones B.J.M., Marra M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=CZECH II; TISSUE-Mammary tumor metastatized to lung. Tumor arose spontaneously;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klauener R.D., Collins F.S., Wagner L., Shermen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K., Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Haleh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
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Stanopus laevis (African clawed frog).
Sukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Annura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024679; AAH24679.1; -; mRNA.
MGI; MGI:2140767; AA536743.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE 143 AA; 15527 MW; 59547DA0P91D5D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49.0%; Score 699; DB 2; 90.9%; Pred. No. 2.8e-45; ive 6; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        223 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 90.9
Matches 130; Conservative
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Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heleh F.,
D. Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
B. Raha S.S., Loquellano N.A., Peters G.J., Abrameon R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Vilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchanko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield X.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 NEANADVLKAMVADNSVVGDTSVFDPESPTTPNTPTSPLPPDTPISPTSPTETPSKHSCR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MGLFGVLICHLLKKKGYRCTTEAEQDIEEEKV--EKIELNDSVNE-NSDTVGQIVHYIMK 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MGLVGVLICHLLKKKGYRCTTEAEPPPVEEKIVGEKIEMHESNGDTNTDTVGHIVNFIMK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  177 GHHLHTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
Richardson P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSURE-Ovary;

Klein S., Strausberg R.;
Submitted (MAY-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC070680; AAH70680.1; -; mRNA.
SEQUENCE 224 AA; 24512 MW; 516BF3010B11D9F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  237 SNOKERRSLMSVSGAETVNGEVPATPVK---RERSGTE 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.0%; Score 641.5; DB 2; Best Local Similarity 63.8%; Pred. No. 1.1e-40; Matches 139; Conservative 21; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 AA
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Name=LOC553285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dev. Dyn. 225:384-391(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse cDNA sequences."
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QSM7X6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUCLEOTIDE SEQUENCE.
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TISSUE=Whole;
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Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
A Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
A Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzhy D.M., Sodergren B.J., Lu X., Gibbs R.A.,
A Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
A Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
T and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            128 EANADVLKAMVADNSL----YDPESPVTPSTPGSP--PVSP-GPLSPGGTPGKHVC-G 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 HHLHTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 HHLHTVGGVAERNACTRCTNKRWHFLKSPQKHKEPRRSHQGAVTVLSVGRFRVTKVEPKS 180
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUB=Ovary;
MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
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Amphibia, Batrachia, Anura, Mesobatrachia, Pipoidea, Pipidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'Genetic and genomic tools for Xenopus research: The NIH Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ch 46.9%; Score 669; DB 2; Length 223; Il Similarity 65.4%; Pred. No. 8.7e-43; 142; Conservative 21; Mismatches 36; Indels 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klein S., Strausberg R.;
Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BCO56115; AAH56115.1; -; mRNA.
SEQUENCE 223 AA; 24273 MW; SEBBCD32032367AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
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NCBI_TaxID=8355;
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QENRQ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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10 QGNRQ3

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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
Alusner R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buerow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
A bitchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
A Stapleton M. J. Usdin T.B., Tooblyuki S., Carninci P., Prange C.,
Brownstein M.J., Usdin T.B., Tooblyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunstrane P.H.,
A Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
A Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B.,
B. Maring M., Anden A., Schein J.B., Jones S.J.M., Marra M.A.,
Schein J.B., Jones J.M., Marra M.A.,
Schein J.B., Jones J.M., Marra M.A.,
Schein J.B., Jones J.M., Marra M.A.,
Schein J.B., Jones S.J.M., Marra M.A.,
Schein J.B., Jones J.M., Marra M.A.,
Schein J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SLYDPESPVTPSTPGSPPVSPGPLSPG--GTPGKHVCGHHLHTVGGVV-ERDVCHRCRHK 198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNQKERRSLMSVSGAETVNGEV 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PDNGSSRTLHSRTETTPSPSNDTGNGHPEYIAYALVPVFFIMGLFGVLICHLLKKKGYRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gapa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tetraodon nigroviridis (Green puffer).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13-SEP-2005 (TrEMBLrel. 31, Created)
13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
Chromosome underermined SCAF14506, whole genome shotgun sequence.
ORFNames=GSTENG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 280;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NIH MGC Project;
Submitted (DEC-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC088389; AAH88389.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   280 AA; 30423 MW; 251CCA8028435E76 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40.7%; Score 581; DB 2;
49.6%; Pred. No. 5.5e-36;
cive 43; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      281 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 49.6
Matches 123; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    259 PATPVKRE 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rissum=Whole;
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-AEQDIEEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPV 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 TPSTPGSPPVSPGPLSPGGTPG--KHVCGHHLHTVGGVVERDVCHRCRHKRWHFI-KPTN 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   64
Maucell E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A., Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B., Dasilva C., Salanoubat M., Levy M., Boudet N., Castellano S., Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B., Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V., Cruaud C., Duprat S., Brottier P., Coutanceau J.P., Gouzy J., Relis M., Volff JN., Guigo R., Zody M.C., Medrico P., Bosak S., Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M., Lauder V., Schachter V., Quetier F., Saurin W., Scarpelli C., Wincker P., Lander E.S., Welsenbach J., Roset Crollius H., "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | : : | || || || || || TAVSQHNATDGKNGGGADGTQPNYVAFVLVPVPFLLGLLGVVICHVLKRKGYRCTTEPQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirata M., Suto Y.,
Hirai M., Terao K., Suzuki Y., Sugano S., Hashimoto K., Kususda J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 TETTPSPSNDTGNG-----HPEYIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain cortex;
MEDLINE=21458551; PubMed=11574149; DOI=10.1016/S0378-1119(01)00665-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MAY-2005 (Rel. 47, Last annotation update)
10-MACCOSIS factor receptor superfamily member 19L precursor (Receptor expressed in lymphoid tissues).
Name-TNFRSF19L; Synonyms-RELT; ORFNames-QccE-10051;
Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota Metazos, Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
Cercopithecidae; Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VC.LEOTIDE SEQUENCE.
Genoscope, Whitehead Institute Centre for Genome Research;
Submitted (FEB-2004) to the EMBL/GenBank/DDBJ databases.
-!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 29.6%; Score 422.5; DB 2; Length 281; Best Local Similarity 46.5%; Pred. No. 6.2e-24; Matches 93; Conservative 33; Mismatches 53; Indels 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAAE01014506; CAF96695.1; -; Genomic_DNA.
VCE 281 AA; 30111 MW; 7B09ACCF514A0325 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  430 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the early vertebrate proto-karyotype.";
Nature 431:946-957(2004).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            177 RKAEQQRRSAGEVTVLAVGR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gene 275:31-37(2001).
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NUCLECTIDE SEQUENCE, PROTEIN SEQUENCE OF N-TERMINUS, AND INTERACTION
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    This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRQPGNGTRAGGPEETAAQYAVIAIVPVFCLMGLLGILVCNLLKRKGYHCTAHKEVGPGP 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------QDIBEEKVEKIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVAD 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             141 NSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVC--GHHLHTVGGV--VERDVCHRCR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ---YHSKQLVQTS---HRPVSKLPPAPPNVP--HICPHRHHLHTVQGLASLSGPCCSRCS 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |:| : | ||||||| :: 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      204 GGGGSGINPAYRTEDV-------NEDTIGVLVRLITEKKENAAALEELLKE 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 HKRWHFI-------KPTNKSRE-SRPRRQGEVTVLSVGRFRVTKVEHKS 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44 TPSPSNDTGNGHPE----YIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAE----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                    FUNCTION: Mediates activation of NF-kappa-B (By similarity). May
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytoplasmic (Potential).
TNFR-Cys.
N-linked (GlcNAc. ..) (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TRIBL HUMAN STANDARD; PRT; 430 AA.

Q96924; Q86V34; Q96JU1; Q9BUX7;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tumor necrosis factor receptor superfamily member 19L precursor (Receptor expressed in lymphoid tissues).
Name=TNFRSE191; Synonyms=RELT;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82;
                                     play a role in T-cell activation.
SUBUNIT: Associates with TRAF! (By similarity).
SUBCELLULAR LOCATION: Type I membrane protein (Probable).
SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor necrosis factor receptor superfamily member 191. Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 309; DB 1; Length 430; Pred. No. 4.2e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BA8DE92593E1E859 CRC64;
                                                                                                                                                                                                                                                                               HSSP; Q92956; LUMA.
InterPro; IPR001368; TNFR_c6.
SWART; SM0208; TNFR; 1.
PROSITE; PS00622; TNFR NGFR 1; FALSE NEG.
PROSITE; PS50050; TNFR NGFR 2; FALSE NEG.
Glycoprotein; Receptor; Signal; Transmembrane.
SIGNAL
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By similarity.
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HSSP; Q92956; 1JMA.
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Gene 278:267-267(2001).
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NCBI_TaxID=9606;
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TISSUE-Blood, Colon, and Eye;

WEDLINE-238827; PubMeda-1247932; DOI=10.1073/pnas.242603899;

RELINE-238827; PubMeda-1247932; DOI=10.1073/pnas.242603899;

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Raha S., Worley A.C., Grimwood J., Schmutz J., Myers R.M.,

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Rudeneration and initial analysis of more than 15,000 full-length human
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R. Ackine M., Obayashi K., Sato H., Nagai K., Kimura K., Makita H.,

R. Schine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,

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R. A Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,

R. Shiratori A., Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H.,

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R. Sugawara M., Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E.,

R. Amazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

R. Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,

R. Pujimori X., Takiguchi S., Watanabe S., Yosida M., Horuta T.,

R. Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,

R. Momiya S., Momiyama H., Satoh N., Takauki S., Sasaki N., Sano S.,

R. Momiyama H., Satoh N., Takani S., Terashima Y., Sarok S.,

R. Momiyama H., Satoh N., Takani S., Terashami Y.,

R. Makagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakabe H.,

R. Marazki M., Watanabe T., Sugiyama A., Itakura S., Fukuzumi Y.,

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R. Kawabata A., Hikili T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,

R. Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,

Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,

R. Matsubima-Sugano J., Satoh T., Shigata K., Sasaki M.,

R. Matsubima-Sugano J., Satoh T., Shizka Y., Sasaki M.,

R. Makashi K., Yada T., Nowura V., Ohara O., Isogai T., Sugano S.;

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TISSUB=Lymphoma; MEDLINB=12313261; DOI=10.1182/blood.v97.9.2702; MEDLINB=21213541; PubMed=11313261; DOI=10.1182/blood.v97.9.2702; Sica G.L., Zhu G., Tamada K., Liu D., Ni J., Chen L.; "RELT, a new member of the tumor necrosis factor receptor superfamily, is selectively expressed in hematopoietic tissues and activates transcription factor NF-kappaB."; plood 97:2702-2707(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nat. Genet. 36:40-45(2004).
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Jikuya H., Tak
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EMBL; AK049073; BAC33534.1; -; mRNA.
EMBL; AK088621; BAC40459.1; -; mRNA.
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                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                    Name=Tnfrsf191
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                                                                                                                                                                                                        -!- SUBUNIT: Associates with TRAFI.
-!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
-!- ISSUB SPECIFICITY: Highest levels are in spleen, lymph node, thymus, peripheral blood leukocytes, bone marrow and fetal liver. Very low levels in skeletal muscle, testis and colon. Not detected very low liver.
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                                                 PROTEIN SEQUENCE OF 26-40.

PubMed=15340161; DOI=10.1110/ps.04682504;

Zhang Z., Henzel W.J.;

"Signal peptide prediction based on analysis of experimentally
verified cleavage sites.";

Protein Sci. 13:2819-2824(2004).

-I-FUNCTION: Mediates activation of NP-kappa-B. May play a role in
                                                                                                                                                                                                                                                                                                       in brain, kidney and pancreas.
SIMILENITY: Contains 1 TNFR-Cys repeat.
CAUTION: Ref.4 sequence differs from that shown due to several
frameshifts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TNFR-Cys.
N-linked (GlcNAc. ..) (Potential)
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/FTId=VAR 022614.
D -> S (in Ref. 4).
K -> E (in Ref. 2).
H -> R (in Ref. 2).
 spleen.";
Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
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Potential.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AK027899; BAB55441.1; -; mRNA.
EMBL; BC001812; -; NOT ANNOTATED CDS; mRNA.
EMBL; BC017279; AAH17279.1; -; mRNA.
EMBL; BC051810; AAH51810.2; -; mRNA.
EMBL; AK074128; BAB44954.1; ALT_FRAME; mRNA.
HSSP; Q92956; 1JMA.
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By similarity.
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EMBL; AK027899; BAB55441.1; -; mRNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC; HGNC:13764; TNFRSF19L.
H-InvDB; HIXO009918; -
InterPro; IPR001368; TNFR_C6.
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REPLINESTIVE SEQUENCE LLARGE SCALE WEARA).

REPLINESZISGEGJ, and NOD; TISSUES-Cerebellum, and Thymus;

REPLINESZISGEGJ, bubMedal246861; DOI=10.1038/nature01266;

REPLINESZISGEGJ, bubMedal24681; DOI=10.1038/nature01266;

RA OKAZAKI Y., FURTUNO M., KABUKAWA T., Adachi J., Bono H., Kondo S.,

RA Nikaido I., OBSTON N., Saltio R., Suzuki H., Yamanaka I., Kiyosawa H.,

RA Agi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,

RA Blake J.A., Brangin A., Mateuda H., Baralov S., Baisel K.W.,

RA Blake J.A., Brangin A., Mateuda H., Baralov S., Baisel K.W.,

RA Baake Land T., Gariboldi M., Gissi C., Godzik A., Frazer K.S.,

RA Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis B.D.,

RA Anai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,

RA Anai A., Kawaji H., Marchionni L., McKenzie L., Miki H.,

RA Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,

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RA Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K.,

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RA Vana Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,

RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,

RA Hara A., Hashizume W., Imotani K., Ishii Y., Itch M., Kagawa I.,

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RA Birney B., Havashizaki Y.,

RA Birney B., Havashizaki Y.,

RA Birney B., Rayashizaki Y.,

Rayashishin A.,

Rayashishin
                                                                                                                                                                197 HKRWHFI-------KPTNKSRE-SRPRRQGEVTVLSVGRFRVTKVEHKS 237
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRIDL MOUSE STANDARD; PRT; 436 AA.
QBBX43; QBBTV0;
13-SEP-2005 (Rel. 48, Created)
13-SEP-2005 (Rel. 48, Last sequence update)
13-SEP-2005 (Rel. 48, Last annotation update)
Tumor necrosis factor receptor superfamily member 19L precursor.
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--- SUBUNT: Associates with TRAFI (By similarity).
--- SUBCATION: Type I membrane protein (Probable).
--- SIMILARITY: Contains 1 TNFR-Cys repeat.
                                                                                                                                                                                                                                                                                                                                                                                         238 NQKERRSLMSVSGAETVN-----GEVPATP 262
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55 HPBYIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTBAEQDIEEEKVEKIELNDSVNENS 114
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Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villadon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smallus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
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STRAIN=CS7BL/6G; TISSUB=Cortex;
MEDLINE=99279253; Pubmed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.,
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
MUB musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830089108 product:hypothetical protein, full insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=C57BL/6J; TISSUE=Cortex; MEDLINE=2108/35055500; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500; Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Arakawa T., Hara A., Pukuniah Y., Komno H., Adachi J., Fukuda Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 294;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 EKRYGLHEHRDGSPTDRSWGSGGGEP--GGSQAAGGGQPRTGT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Indels
                                                                                                                                                                                                                                                                                                                                     TISSUE=Eye;
Strausberg R.;
Strausberg (OCT-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31456 MW; BASDEDE20243EAF6 CRC64;
                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
20.3%; Score 289; DB 2;
Best Local Similarity 38.4%; Pred. No. 9.1e-14;
Matches 86; Conservative 28; Mismatches 82.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         303 AA
                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, BC038500; AAH38500.1; -; mRNA.
Ensembl; ENSMUSG0000044024; Mus musculus.
MGI; MGI:1918044; 4631403P03Rik.
                                                                                                                                                                                                                                                and mouse cDNA sequences."
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                                                                                                                                                                                                                                                                                                                      NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         294 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 VADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKHVC--GHHLHTVGGV--VERDVCH 193
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gape
                                                                                                                                                                                                                                                                                                                                                                                         N-linked (GlcNAc. . .) (Potential)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20.7%; Score 295.5; DB 1; Length 436;
                                                                                                                                                                                                                                           Tumor necrosis factor receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Pred. No. 4.5e-14;
36; Mismatches 89; Indels
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1F96C5E021945DF9 CRC64;
                                                                                                                                                                                                                                                                                          Extracellular (Potential).
                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential). TNFR-Cys.
                                                                                                                                                                                                                                                                       superfamily member 19L.
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Last annotation update)
                   Ensembl; ENSMUSGG000008318; Mus musculus.
MGI; MGI:444373; Thfrsf191.
GO; GO:0016021; C:integral to membrane; TAS.
InterPro; IPR001368; TNFR_GC.
SWART; SM00208; TNFR; 1.
PROSITE; PS00652; TNFR NGFR 1; PALSE NEG.
PROSITE; PS50050; TNFR NGFR 2; PALSE_NEG.
Glycoprotein; Receptor; Signal; Transmembrane.
SIGNAL
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By similarity.
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01-MAR-2003 (TrEMBLrel. 23,
01-MAR-2004 (TrEMBLrel. 26,
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Q8CFT0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82; Conservative
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01-MAR-2004 (TrEMBLrel.
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TRANSMEM
TOPO DOM
REPEAT
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28; Gaps

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Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuehl P., Lewis S., Marsuo Y., Gissi C., King B., Kochiwa H.,
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Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P.,
Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Satorch K.-F.,
Wunnbaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
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Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P., Pukuda S., Puruno M., Hanagaki T., Hara A., Hashizume W., Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T., Hori' F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T., Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S., Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M., Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y., Saltoh H., Sakai C., Sakai K., Shizaki T., Sogabe Y., Tagami M., Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T., Tomaru A., Toya T., Yawunishi A., Muramatsu M., Hayashizaki Y., Submitted (JUL-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C57BL/6J; TISSUB=Cortex,
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazadi Y., Muramatsu M., Hayashizaki Y.;
"Normalization and subtraction of cap-trapper-selected cDNAs to
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MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Alzawa K., Nagaoka S., Sasaki N., Carninci P.,
Konno H., Akiyama J., Nishi K., Kiteunai T., Tashino H., Itoh M.,
Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harda A.,
Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
Pujiwake S., Inoue K., Togawa Y., Izawa M., Ohara B., Watahiki M.,
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,
"RIKEN integrated sequence analysis (RISA) system-384-format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 protein.
303 Aa; 32326 MW; 06287A05AA64793B CRC64;
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MGI; MGI:1918044; 4631403P03Rik.
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The FANTOM Consortium,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Res. 10:1757-1771(2000)
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           RANGE BERKER BER
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TISSUE-Whole body;

X Straubberg R.L.; Feligold B.A.; Grouse L.H.; Derge J.G.;

A Straubberg R.L.; Feligold B.A.; Grouse L.H.; Derge J.G.;

A Rauberg R.L.; Feligold B.A.; Grouse L.H.; Derge J.G.;

A Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

A Altschul S.F.; Zeeberg B., Buetow K.H.; Schaefer C.F.; Bhat N.K.;

Hopkins R.F.; Jordan H.; Moore T., Max S.I.; Wang J., Heich F.;

A Bratchench C., Marusina K.F.; Farmer A.A.; Rubin G.M.; Hong L.;

A Brownstein M.J.; Usdin T.B.; Toshiyuki S., Carninci P.; Prange C.;

A Raha S.S.; Loquellano N.A.; Peters G.J.; Abramson R.D.; Mullahy S.J.;

B Bosak S.A.; Morley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.J.;

A Kichards S.; Worley K.C.; Hale S.; Garcia A.M.; Gay L.J.; Hulyk S.W.;

A Nilalon D.K.; Muzny D.M.; Sodergren E.J.; Lu X.; Gibbs R.A.;

Raha S.S.; Caudelland N.A.; Sodergren E.D.; Dickson M.C.;

A Miting M.; Madan A.; Young A.C.; Shevchenko Y.; Bouffard G.G.;

B Blakesley R.W.; Touchman J.W.; Green E.D.; Dickson M.C.;

B Rotiguez A.C.; Grimwood J.; Schmutz J.; Myers R.M.;

B Cherration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58 YIAYALVPVFFIMGLFGVLICHLLKKKGYRCTT-----EAEQDIBEEKVEKIELNDSV 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              111 NENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTP-----STPGSPPVSPG 163
HPEXIAYALVPVFFIMGLFGVLICHLLKKKGYRCTTBABQDIBBEKVBKIELNDSVNENS 114
                                                                                      174
                                                                                                            70 DIVERIVECIIQNEANAEALKEMLGDS---EGEGTYQLSS----VDATSSLQDGAPSHH 121
                                                                                                                                                                                                                122 -----HTVHLGSAAPCIHCSRSKRPPLVRQGRSKEGKSRP-RPGETTVFSVGRFRVTHI 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 HGLYMLFLLVLVFPLMGLVGFMICHVLKKKGYRCRTSRGSEPDDAQLQPPE-DDDVNE-- 69
                                                                                      DIVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPGKH
                                                                                                                                                                        175 VCGHHLHTVGGVVERDVCHRCRHKRWHFIKP-TNKSRESRPRRQGEVTVLSVGRFRVTKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20.3%; Score 289; DB 2; Length 325; 35.0%; Pred. No. 1e-13; ive 30; Mismatches 62; Indels
                                                                                                                                                                                                                                                           234 -----EHKSNQKERRSLMSVSGAETVNGEVPATPVKRERSGT 270
                                                                                                                                                                                                                                                                                                   175 EKRYGLHEHRDGSPTDRSWGSGGGQEP--GGSQAAGGGQPRTGT 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Klein S., Gerhard D.S.;
Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; BC075421; AAH75421.1; -; mRNA.
Ensembl; ENSETG00000002622; Xenopus tropicalis.
SEQUENCE 325 AA; 36517 MW; 69129BF0CE1B18CB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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les 82, Conservative
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QGDIW4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGC89179 protein.
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Matches
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Gaps

28;

20.3%; Score 289; DB 2; Length 303; 38.4%; Pred. No. 9.4e-14; ive 28; Mismatches 82; Indels ;

Conservative

Best Local Similarity Matches 86; Conserva

Query Match

	Ltd.
5.1.7	Biocceleration
version	- 2006
SenCore	(c) 1993
ger	ΰ
	opyright

OM protein - protein search, using sw model

Run on:

February 23, 2006, 12:04:08; Search time 40 Seconds (without alignments) 651.869 Million cell updates/sec

US-10-620-562-2 Title: Perfect score:

1 MAPRALPGSAVLAAAVFVGG......ETVNGEVPATPVKKERSGTE 271 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 283416 segs, 96216763 residues Searched:

283416

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	cell surface glyco	surface protein -	genome polyprotein	heterocyst glycoli	cell adhesion 80K	urPAB protein prec	testicular zinc fi	hypothetical prote	transcription fact	hypothetical prote		•	laminin alpha-1 ch	genome polyprotein	hypothetical prote	hypothetical prote	E-box-binding prot	EF protein - Strep	dap	EF protein - Strep	cell adhesion mole	basic helix-loop-h	retinoid-X-recepto	probable protein k	transcription fact	hypothetical prote		microtubule-associ	genome polyprotein
SUMMARIES	a	JC2300	T30271	S47508	AG2474	A31643	855377	JC7316	T00359	A42121	T46444	T25236	S47633	MMMSA	GNVSPD	T29774	AB2504	A46691	S33442	T13946	S33441	A44100	S19958	A43781	T02414	T13751	T16157	S48940	AS6577	GNVSPP
	B	7	~	7	N	7	7	7	7	7	~	7	~	Н	н	~	~	7	~	~	~	~	~	~	~	N	7	~	7	Н
	Match Length	1083	1679	3140	1541	514	345	942	634	682	1062	349	452	3084	3141	120	513	707	843	1199	1822	514	206	467	612	2061	512	605	2364	3125
& Query	Match	7.4	7.3	6.9	6.9	6.8	6.8	6.8	6.7	9.9	9.9	9.9	9.9	9.9		6.5	6.4	6.4	6.4	6.4	6.4	6.4	6.4	6.3	6.3	6.3	6.2	6.2	6.2	6.2
	Score	105.5	104.5	98.5	97.5	97	96.5	96.5	95.5	94	94	93.5	93.5	93.5	92.5	92	91.5	91.5	91.5	91.5	91.5	91	91	S.	89.5	•	89	89		83
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MCX1 related prote membrane conserved	retinoid X recepto excinuclease ABC c	All-1 protein +GTE partial CDS - Caen	fibronectin-bindin	SRB9 protein - yea	initiation factor-	translation initia	hypothetical prote	shed acute-phase a	DNA ligase (ATP) (dihydrolipoamide S	hypothetical prote
T49681 H90429	I50515 AG3314	A48205 T29144	819702	B57062 R81576	E86530	F72093	B96803	823006	148921	B55514	T16368
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563 355	441 909	3869	940	1420	890	890	232	879	916	553	759
6.2	6.2	6.2	6.1	1.9	6.1	6.1	6.1	6.1	6.1	6.0	0.9
88.5 88	8 8 8 8	8 8	87.5	87.5	87	87	86.5	86.5	86.5	86	98
30	33	3.4 3.5	36	37	38	40	41	42	43	44	45

ALIGNMENTS

A;Gene: MSG100 C;Superfamily: Pneumocystis carinii major surface glycoprotein MSG100 C;Keywords: glycoprotein

Indels 37; Gaps Query Match 7.4%; Score 105.5; DB 2; Length 1083; Best Local Similarity 25.3%; Pred. No. 2.5; Matches 37; Conservative 22; Mismatches 50; Indels 37;

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71 GLFGVLICHLLKKKKGYRCTT----EAEQDIEBEKVEKIELNDSVNENSDTVGQIVHYI 124 125 MK-----NEANADVLKAMVADNSLYDPESPVTPSTPGSP----PVSPG-----163 164 -PLSPGGTPGKHVCGHHLHTVGGVVE 188 ઠે g ò 셤 ò

854 TPGTPGGAPG-----TPGGMMK 870 셤

RESULT 2

surface protein - fluke (Schistosoma mansoni)

Cypecies: Schistosoma mansoni
Cypecies: Schistosoma mansoni
Cypecies: Schistosoma mansoni
Cypecies: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
Cypecies: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 09-Jul-2004
Cypecies: 02-Sep-2000 #sequence_revision 02-Sep-2000
Exp. Parasitol. 80, 242-249, 1995
Exp. Parasitol. 80, 242-249, 1995
Exp. Parasitol. 80, 242-249, 1995
AyTitle: Schistosoma mansoni: molecular cloning and sequencing of the 200-kDa chemothera
AyReference number: 220800; MUID:95203407; PMID:7534724
AyReference number: 220800; MUID:95203407; PMID:7534724
AyRecession: T30271
AyRe

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heterocyst glycolipid synthase [imported] - Nostoc sp. (strain PCC 7120)
C;Species: Nostoc sp. PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
A;Note: Nostoc sp. strain PCC 7120
C;Accession: AG2474
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriguchi Nakzaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S. A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anah, A;Reference number: AB1807; MUID:21595285; PMID:11759840
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R;Kamboj, R.K.; Wong, L.M.; Lam, T.Y.; Siu, C.H.
J. Cell Biol. 107, 1835-1843, 1988
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A; Residues: 1-514 <KRM>
A; Cross-references: UNIPARC:UP100001284F3; GB:M36545; NID:g167803; PIDN:AAA33212.1; PID:s
RNoegel, A.; Gerisch, G.; Stadler, J.; Westphal, M.
EMBO J. 5, 1473-1476, 1986
A; Title: Complete sequence and transcript regulation of a cell adhesion protein from aggs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: Lowns
A;Molecule type: Lowns
A;Residues: 1-1541 <KURs
A;Cross-references: UNIRKOT:Q8YLE7; UNIPARC:UPI00000CEE52; GB:BA000019; PIDN:BAB77050.1;
A;Experimental source: strain PCC 7120
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A,Reference number: A31643; MUID:89034443; PMID:3182938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----APVAAPAIDVADLDKNLLAIISDKTGYPVEMLELEMDMEADLGIDSIKRVEIL 1349
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1541;
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Local Similarity 21.3%; Pred. No. 17;
tes 45; Conservative 30; Mismatches
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A, Status: preliminary
A, Molecule type: DNA
A, Residues: 1-514 < DES>
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    MN 2939
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Best Local S
Matches 45
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A; Residues: 1-3140 «MAL>
A; Residues: 1-3140 «MAL>
A; Residues: 1-3140 «MAL>
A; Cross-references: UNIPRO: (Q84925; UNIPARC: UPI00000F3F01; EMBL: X81083; NID: 9531731; PID
A; Experimental source: 1801are PVV-SC
C; Superfamily: tobacco etch virus genome polyprotein
C; Superfamily: tobacco etch virus genome-linked protein; nucleotide binding; P-loop; phosph
F; 1-308/Product: protein P1 #status predicted «HE>
F; 109-76/Product: protein P3 #status predicted «PIP>
F; 107-1116/Product: protein F3 #status predicted «AIP>
F; 116-1803/Product: protein GK1 #status predicted «AIP>
F; 115-1803/Product: protein GK1 #status predicted «CIP>
F; 125-126/Region: nucleotide-binding motif A (P-loop)
F; 1343/Region: DEXH motif.
F; 1347-1345/Region: DEXH motif.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 ADNSLYDP----ESPVTPSTPGSPPVSPGPLSPGGTPGKHVCGHHLHTVGGVVERDVCH 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           194 RCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNQKERRSLMSVSGAET 253
                                                                                                                                                                                                                                          EDIKGAGLSLTVEGIHHNHETQETELDVAVHIASKVISDNIACRPTYLLLEFIEPNIETL 807
                                                                                                                                                                                     ----AEQDIEEEKVEKIELNDS--VNENSDTV-- 117
                                                                                                                                                                                                                                                                                                                                                                      ----GQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPVSPGPLSPGGTPG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KHVCG-----HH-----THTVGGVVERDVCHRCRHKRWHFIKP---TN 207
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                                                                                               69
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         Length 1679;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KSRESR-----PRROGEVTV---LSVGRFRVTKVEHKSNQ 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       851
                                                                                          73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fil34z-13% Region: Dean mout.
Fil804-1286/Product: protein 6K2 #status predicted <6K2.
Fil807-2292/Product: protein NIa #status predicted <NIA.
Fil857-2049/Product: VPg protein #status predicted <VPG-
Fi2293-2810/Product: protein NIb #status predicted <NIB.
Fi2811-3140/Product: coat protein #status predicted <NIB.
         DB 2;
    7.3%; Score 104.5; D
22.8%; Pred. No. 5.2;
[ve 31; Mismatches
                                                                                                                                                                                     79 HLLKKKGYRCTTE------
                                               22.8%;
                                                                                          51; Conservative
Query Match
Best Local Similarity
Matches 51; Conserv
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A;Cross-references: UNIPROT:Q51932; UNIPARC:UP100000AE87E; EMBL:248975; NID:g854370; PID:
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R;Inoue, A.; Ishlji, A.; Kasagi, S.; Ishlzuka, M.; Hirose, S.; Baba, T.; Hagiwara, H.
Biochem. Biophys. Res. Commun. 273, 398-403, 2000
A;Title: The transcript for a novel protein with a zinc finger motif is expressed at A;Reference number: JC7316
A;Contents: Testis
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C;Keywords: meiosis; spermatogenesis; testis; transcription regulation; zinc finger
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C;Comment: This protein, with a zinc finger motif, functions as a transcriptional
in the initiation of the reduction divisions of meiosis and/or in the maintenance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----GGIPGKHVCGHHLHTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEV 220
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                                                                                                        C;Species: Peptostreptococcus magnus
C;Species: 15-Jul.1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C;Accession: SS5377
R;de Chateau, M.; Bjoerck, L.
R;de Chateau, M.; Bjoerck, L.
A;Description: Protein urPAB.
A;Reference number: SS5377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     testicular zinc finger protein - mouse
C;Species: Mus musculus (house mouse)
C;Date: 08-Sep-2000 #sequence_revision 08-Sep-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 EEEKAKKEAEKOVSDSWYDOSKHPFAYRTKEEAEQAAKKAL--ENELLNPGHINNSYKVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 QKYDGNWEYVLSPNLABTPETPKKPSKPDVTPNPSTPEVEEKDPVLPSYPRLDNHYFMNG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97 EBEKVEKI BLNDSVNENSDTVGQI VHY I MKNEANADVLKAMVADNSLYDP---
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                                                                                   - Peptostreptococcus magnus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6.8%; Score 96.5; DE Alarity 20.3%; Pred. No. 3.2; Conservative 17; Mismatches
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llarity 21.4%; Pred. No. 11;
Conservative 39; Mismatches
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Best Local Similarity
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les 75; Conserv
                                                                                   urPAB protein precursor
                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-345 <DEC>
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A; Residues: 1-942 <INO>
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A; Molecule type: protein
A; Accession: S01473
A; Molecule type: protein
A; Recession: S01473
A; Molecule type: protein
A; Redeaus: 20-37, "X', 39-41, "X', 43-46 <STA>
A; Cross-references: UNIPARC:UF1000017B17B
B; Stadler, J.; Keenan, T.W.; Bauer, G.; Gerisch, G.
EMBO J. 8, 371-377, 1989
A; Fittle: The contact site A glycoprotein of Dictyostellum discoideum carries a phospholi
A; Reference number: A56857; MUD:89251561; PMID:2721485
A; Contents: annotation; detection of glycosphingolipidinositol and ceramide were
A; Note: no phosphoserine was detected but phospholiositol and ceramide were
A; Note: the N-linked carbohydrates are sulfated type 1 oliqosaccharides
C; Comment: This protein is involved in the formation of intercellular contacts upon aggr
C; Comment: This protein is involved in the formation of intercellular contacts upon aggr
C; Genetics:
A; Gene: csA
C; Keywords: blocked carboxyl end; cell adhesion; glycoprotein; lipoprotein; membrane prof
F; 132-139/Region: cell adhesion #status predicted
F; 20-514/Pomain: signal adhesion #status predicted
F; 492-179/Region: cell adhesion #status predicted
F; 492-179/Region: cell adhesion #status predicted
F; 492/Modified site: GSI-anchor ethanolamine amidated carboxyl end (Ser) (in mature form
A;Reference number: A26310
A;Accession: A26310
A;Accession: A26310
A;Molecule type: mRNA
A;Residues: 1-215,'G',217-514 <NOE>
A;Cross-references: UNIPARC:UPI000016B99B; EMBL:X04004; NID:g7246; PIDN:CAA27634.1; PID:
A;Cross-references: UNIPARC:UPI000016B99B; EMBL:X04004; NID:g7246; PIDN:CAA27634.1; PID:
Broc. Natl. Acad. Sci. U.S.A. 83, 4248-4252, 1986
A;Title: Cloning of CDNA for the contact site A glycoprotein of Dictyostelium discoideum
A;Reference number: A23951
                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 20-49 < MON>
A; Residues: 20-49 < WON>
A; Residues: 20-49 < WON>
A; COSS-references: UNIPARC: UPI0000000031; GB: M13546; NID: g167699; PIDN: AAA33181.1; PID: R; Kamboj, R.K.; Gariepy, J.; Siu, C.H.
Cell 59, 615-625, 1989
A; Title: Identification of an octapeptide involved in homophilic interaction of the cell A; Reference number: A33463; MUID: 90058644; PMID: 2582489
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A;Molecule type: protein
A;Residues: 132-139 «KA2>
A;Residues: 132-139 «KA2>
A;Cross-references: UNIPARC:UPI000017B17A
B;Stadler, J.; Bordier, C.; Lottspeich, F.; Henschen, A.; Gerisch, G.
Hoppe-Seyler's Z. Physiol. Chem. 363, 771-776, 1985
A;Title: Improved purification and N-terminal anino acid sequence determination of A;Reference number: S01473; MUID:83005404; PMID:7118072
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GG----TPGKHVCGHHLHTVGGVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVL 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGKYFVTTASVTMGSHIYT--GLTVQDDGTNC----HVIFTTRSVYES----SNTITAK 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 VFVGGAVSSPLVAPDNGSSRTLHSRTETTPSPSN------DTGNGHPBYIAYAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gabs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            224 SVGRFRVTKVEHKSNOKE---RRSLMSVSGAETVNGEVPATPVKRERSGTE 271
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19.6%; Pred. No. 4.8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STIPPNNGRIGMILVDGPSNISGY-----
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Matches 57; Conserva
                                                                                                                                                                                                                                                                                                               A; Accession: A23951
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C;Genetics:
A;Note: DKFZp434N1427.1
                                                                                                           A; Molecule type: mRNA
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R,Bloecker, H.; Boec
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: GDB:TCF12
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transcription factor HTF4 - human

lyalternate names: helix-loop-helix protein (HEB)

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 31-Dec-1993 #sequence revision 31-Dec-1993 #text_change 09-Jul-2004

C;Accession: A42121; B56611; B34423; B34424

R;Hu, J.S.; Olson, E.N.; Kingston, R.E.

Nol. Cell. Biol. 12, 1031-1042, 1992

A;Title: HEB, a helix-loop-helix protein related to E2A and ITF2 that can modulate the E A;Reference number: A42121; MUID:92186835; PMID:1312219

A;Accession: A42121

A;Molecule type: mRNA

A;Residues: 1-682 < HUI>

A;Cross-references: UNIPROT:Q99081; UNIPARC:UPI000003B45E; GB:M80627; NID:g183929; PIDN:
                                                                                                                                                                                                                                                                                                              hypothetical protein KIAA0680 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 0.1-feb-1999 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004
C;Accession: T00359
R;Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N. DNA Res. 5, 169-176, 1998
A;Title: Prediction of the coding sequences of unidentified human genes. X. The complete A;Reference number: Z14142; MuID:98403880; PMID:9734811
A;Accession: T00359
A;Accession: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-634 <ISH>
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C;Genetics:
                                                                                                             344 RSFPDIEDEEKFLYGDEEEDIKSESPLKSLEDPESAGTROKANSLPSTPAVKLESLEE-S 402
                                                                                  170 TPGKHVCGHHLHTVG---GVVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVG 226
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  --PSTPGSPPVSPGPLSPGG 169
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                                                                                                                                                                     227 RF----RVTKVEH-----KSNQKERRSLMSVSGAETVNGEV----PATPV 263
                                                                                                                                                                                                  Length 634;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.7%; Score 95.5; DB 2;
19.5%; Pred. No. 8.2;
tive 24; Mismatches 79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         276 TSHLSSDTTTSGTSDLKGEPAETRVE 301
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A;Residues: 1-682 <a href="https://doi.org/10.1000/19458">https://doi.org/10.1000/19458</a>; GB:M83233; NID:g2243159; PIDN:AAB62389.1; PID A;Cross-references: UNIPARC:UPI0000038458; GB:M83233; NID:g2243159; PIDN:AAB62389.1; PID A;Cross-references: UNIPARC:UPI000038458; GB:M018:11868, NCBIP:118873)
A;Note: it is uncertain whether Met-1, Met-26 is the initiator
R;Zhang, Y:; Babin, J:; Feldhaus, A.L.; Singh, H.; Sharp, P.A.; Bina, M.
A;Zhang, Y:; Babin, J; Peldhaus, A.L.; Singh, H.; Sharp, P.A.; Bina, M.
A;Title: HTP4: a new human helix-loop-helix protein.
A;Reference number: S34423; MUID:91360364; PMID:1886779
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A;Reference number: Z23032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 HDRLSYPPHSVSPTDINTSLPP----MSSF-----HRGSTSSSPYVAASHTPP 315
                                                               ........ and nucleotide sequence of the human transcription factor HTF4a cDNA. A;Reference number: A56611; MUID:93076001; PMID:1446075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PSPKPPTSMFASTFFMQDGTHNSSDLWSSSNGMSQPGFGGILGTSTSHMSQSSSYGNLHS 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------PBY1AYALVPVFFIMGLFGVLICHLLKKKGYRCTTEAEQDIEEEKVEK 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                316 INGSDSILGTRGNAAGSSOTGDALG------KALA---SIXSPDHTSSF 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             104 IELNDSV------NENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPE--SPVT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSTPGSPPVSPGPLS-----PGG-TPGKHVCGHHLHTVGGVVE-----RDVCHRCRH 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---HAVGPSTSLPAGHSDIHSLLGPSHNAPIGSLNSNYGGSSLVASSRSASMVGTHREDS 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 PRALPGSAVLAAAVFV--GGAVSSPLVAPDNGSSRT----LHSRTETTPSPSNDTGNGH- 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Homo sapiens (man)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 6.6%; Score 94; DB 2; Length 682;
Best Local Similarity 20.6%; Pred. No. 12;
Matches 73; Conservative 38; Mismatches 109; Indels 134; Gaps
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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1062 <AAA>
A;Cross-references: UNIPROT:Q9NSW2; UNIPARC:UPI00006FB55; EMBL:AL137701
A;Experimental source: adult testis; clone DKFZp434N1427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214 PRROGEVTVL-SVGRFRVTKVEHKSNOKERRSLMSVSGAETVNGEVPATPVKRE 266
sequence extracted from NCBI backbone (NCBIN:88251, NCBIP:88254)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 570-655 <ZH2>
A;Cross-references: UNIPARC:UP10000176417; EMBL:M65209
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: 15q21-15q21
C;Superfamily: human transcription factor 3
C;Keywords: DNA binding; transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein DKFZp434N1427.1 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GDB:355444; OMIM:600480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        198 KRWHFIKPTNK-----
                                      R;Zhang, Y.; Bina, M.
DNA Seq. 2, 397-403, 1992
A;Title: The nucleotide se
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laminin alpha-1 chain precursor - mouse N;Alternate names: laminin chain Al C;Species: Mus musculus (house mouse)
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                                                                                                                    Query Match
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8X7633
RXR protein - African clawed frog
RXR protein - African clawed frog
C;Species: Xenopus laevis (African clawed frog)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: 847633
R;Marklew, S.; Smith, D.P.; Mason, C.S.; Old, R.W.
Biochim. Biophys. Acta 1218, 267-272, 1994
A;Title: 180lation of a novel RXR from Xenopus that most closely resembles mammalian RXR
A;Reference number: 847633
A;Accession: 847633
A;Accession: S47633
A;Gratus: preliminary
A;Residues: 1-452 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-349 <WIL>
A;Cross-references: UNIPROT:002333; UNIPARC:UPI00007ED28; EMBL:Z81131; PIDN:CAB03425.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6
                                                                                                                         92 AEQDIEEEKVEKIELNDSVNENSDTVGQIVH----YIMKNEANADVLKAMVADNSLYDPE 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 SPVTPSTPGSPPVSPGPLSPGGTPGKHVCGHHLHTVGGVVZR------DVCHRC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 RHKRWHFI-------KPINKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNQK 240
                                                                                                                                                                                                                                      QPEITPS-PLOPPAAPAPTSTTSSARRRAYCRNRDHFATIRTASLVSRQI---QEHEQDS 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APNTPPVPVPPPVQQPQASPNASP------VSVLRRRRYANPEQERFGDISRRI 113
                                                                                                                                                                                         SP-VTPSTPGSPPVSPGPLSPGGTPGKHV-CGH--HLHTV--GGVVERDVCHRCRHKRWH 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEVDLEQOR-RALEMPEQ-QMNDQAFAQLIHDHDVQHINNDAN-------QVPA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25236
R;Cummings, P.
                                                                                              EAEQDIEEEKVEKIELND--SVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLY-DPB
                                                                                                                                                                                                                                                                                     202 FIKPTNKSRESRPRRQGEVTVLSV-GRFRVTKVEHKSN-QKERRSLMSVSGAE 252
                                                                                                                                                                                                                                                                                                                   26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 -HNPANQIPAAPNTQPEVPPTVQQPESSSQERASPTSPEITIFSTGLLGL--
Query Match 6.6%; Score 94; DB 2; Length 1062; Best Local Similarity 26.0%; Pred. No. 21; Matches 45; Conservative 34; Mismatches 68; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Score 93.5; DB 2;
; Pred. No. 5.7;
32; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein T24D1.3 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Accession: T25236
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data Library, October 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 ERRSLMSVSGAETVNGEVPATPVKRER 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Experimental source: clone T24D1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 19.8%;
Matches 41; Conservative 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: Z20001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: 1
A;Introns: 29/2; 298/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C,Genetics:
A,Gene: CBSP:T24D1.3
A,Map position: 1
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                                                                                                                                          208
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A;Note: the sequence from Fig. 2 is inconsistent with that from Fig. 1 in having 118-His C.Superfamily: retinoic acid receptor alpha; erbA transforming protein homology C;Keywords: zinc finger F;126-368/Domain: erbA transforming protein homology <ERBA>
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; Cross-references: UNIPROT:P19137; UNIPARC:UP100000278CA; EMBL:J04064; NID:g309419; PID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Molecule type: protein
A;Residues: 183-195;570-571,'A',573-586;596-612,'X',614-617,'EMK';630-646;1217-1222,'YPP
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SA2>
2486;2624-2639;2818-2843;3009-3033,'V',3035 <SA2>
2486;2624-2629;UNIPARC:UPI0000173C99;UNIPARC:UPI0000173C93;UNIPARC:UPI0000173C94;
C99;UNIPARC:UPI0000173C94;UNIPARC:UPI0000173C98;UNIPARC:UPI0000173C9C;UNIPARC:UPI0000173C9C
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A;Cross-references: UNIPARC:UPI000016CE8F; EMBL:X07737; NID:g52857; PIDN:CAA30561.1; PID
A;Accession: A30450
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A;Residues: 311-335,'N',337-339;630-642,'D',644;692-734;737-748,'X',750-760,'G',762-763;
3-1389;1449-1459 <HA2>
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C;Accession: A31771; A30499; S00624; A30450; S08899; S02678; S01790; A30451; S14670
C;Accession: A31771; A30499; S00624; A30450; S08899; S02678; S01790; A30451; S14670
B;Sasaki, M.; Kleinman, H.K.; Huber, H.; Deutzmann, R.; Yamada, Y.
J. Biol. Chem. 263, 16536-16544, 1988
A;Title: Laminin, a multidomain protein. The A chain has a unique globular domain and A;Reference number: A31771; MUID:89034134; PMID:3182802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----DVKPPLGMRSMQSHP------NGGTVSGKRLCAICGDRSSGKHYGVHSCEGCKGF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 NSLYDPESPVTPSTPGSPPVSPGPLSPGGT-PGKHVC-----GHH--LHTVGG---- 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28 APDNGS-SRTL-HSRTETTPSPSNDTGNGHPEYIAYALV-----PVFFIMGLFGVLICHL 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---VVERDVCHRCRHKRWHFIKPTNKSRESRPRRQGEVTVLSVGRFRVTKVEHKSNQKER
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Mur. J. Batochem. 173, 629-635, 1988
.;Ttle: The N terminus of Laminin A Chain is homologous to the B chains.
s;Reference number: S00624; MUID:88225080; PMID:3267223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.6%; Score 93.5; DB 2; Length 452; 23.0%; Pred. No. 7.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97;
                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 23.0%; Pred. No. 7.8; Matches 60; Conservative 37; Mismatches
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16;

Gaps

201

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genome polyprotein - plum pox virus (strain D)
N;Contains: 29K protein; 34K protein; coat protein (capsid protein); cylindrical inclusic C;Species: plum pox virus; PpV
C;Species: plum pox virus; PpV
C;Species: plum pox virus; PpV
C;Spacession: S06929; JA0078
R;Teycheney, P.Y.; Tavert, G; Delbos, R.; Ravelonandro, M.; Dunez, J.
Nucleic adds Res: 17, 10115-10116, 1989
A;Title: The complete nucleotide sequence of plum pox virus RNA (strain D).
A;Reference number: S06929; MUID:90098790; PMID:2602121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A.Accession: JA0078
A.Accession: JA0078
A.Molecule type: genomic RNA
A.Residues: 2709.'QT'.2714,2810-3141 <RAV>
A.Residues: 2709.'QT'.2712,'L'.2714,2810-3141 <RAV>
A.G. Sessidues: 2709.'QT'.2712,'L'.2714,2810-3141 <RAV>
A.Cross-references: UNIPARC:UPI0000170FC8; GB:D00228; NID:g222410; PIDN:BAA00210.1; PID:gANOte: part of this sequence, including the amino end of the mature protein, was confirmally tobacco etch virus genome polyprotein
G.Keywords: ATP; coat protein; cylindrical inclusion protein; genome-linked protein; inclifical and Product: 34K protein #status predicted <RRO>
F;1-301/Product: helper component protein #status predicted <RCP>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2724 OFGLSONSHLVLPINQSDVRKRLQVQLSIRTFASSGLIYYVAHQNQMDYATLQLQEGRLH 2783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          202 PIKPTNKSRE--SRPRRQGEVTVLSVGRFRVTKVEHKSNQKERRSLMSVSGAE----TVN 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     60 AYALVPVFFIMGLFGVLICHL-----LKKKGYRCTTBAEQDIEEEKVEKIE----LND 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cross-references: UNIPROT:P13529; UNIPARC:UP10000174B40; EMBL:X16415; Ravelonandro, M.; Varveri, C.; Delbos, R.; Dunez, J. Gen. Virol. 69, 1509-1516, 1988; Title: Nucleotide sequence of the capsid protein gene of plum pox potyvirus.; Reference number: JA0078
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6.6%; Score 93.5; DB 1; Length 3084;
Best Local Similarity 22.2%; Pred. No. 85;
Matches 69; Conservative 33; Mismatches 94; Indels 115,
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A;Molecule type: genomic RNA
A;Residues: 1-3141 <TEY>
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                                                                                                                                                                                F;2134-3084/Domain:
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A, Recidue Type: protein
A, Mccession: S14670
A, Recidues: S14670
A, Recidues: A242-2456;2440-2451;2461-2467;2487-2552;2550-2557;2561-2593;2600-2610;2616-2942
A, Rocession: S14670
A, Residues: S242-2456;2940-29576;293000; 17: 3002-3014, 1002-3013, 3002-3014
A, Residues: S242-2456;2940-29576;293000;17: 3002-3014, 1002-3014, 1002-3014
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A; Residues: 153-169 A,RAN>
A; Cross-references: UNIPARC:UPI0000173CAD
R; Pujiwara, S.; Shinkal, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
B; Pujiwara, S.; Shinkal, H.; Deutzmann, R.; Paulsson, M.; Timpl, R.
B; Cochem. J. 252, 453-461, 1988
A; Title: Structure and distribution of N-linked oligosaccharide chains on various domain A; Reference number: $02678; MUID:88326259; PMID:2458101
A; Recession: $03678
A; Molecule 'type: protein
A; Residues: $030-662, 'D', 644; 2690-2704 < FUJ>
A; Cross-references: UNIPARC:UPI0000173CA4; UNIPARC:UPI0000173CAE
R; Deutzmann, R.; Huber, J.; Schmetz, K.A.; Oberbacumer, I.; Hartl, L.
Eur. J. Biochem. 177, 35-45, 1988
A; Pudies: Structural study of long arm fragments of laminin. Evidence for repetitive C-te
A; Reference number: $01790; MUID:89030693; PMID:3181157
A; Accession: $01790
A; Molecule type: mRNA
A; Residues: $2538-3084 < DEU>
A; Accession: $2538-3084 < DEU>
A; Accession: $2538-3084 < DEU>
A; Accession: A; Aptesion A;
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A; Residues: 191-1929; 1997-2006; 2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105; 2120
A; Residues: 191-1929; 1997-2006; 2033-2045, 'X', 2047-2054, 'X', 2056-2066, 'X', 2068-2105; 2120
A; C298-3005, 'A', 3007-3033, 'V', 3035; 2561-2591, 2082-2055; 3005, 'A', 3007-3033, 'V', 3035; 3068-3083, cBE2-
A; Cross-references: UNIPARC: UP10000173CB6; UNIPARC: UP10000173CB7; UNIPARC: UP10000173CB6; UNIPARC: UP10000173CC6; UNIPARC: UP10000173CC6; UNIPARC: UP10000173CC6; UNIPARC: UP10000173CC6; UNIPARC: UP10000173CC9; UNIPARC: UP10000173CC9; UNIPARC: UP10000173CC9; UNIPARC: UP10000173CC6; UNIPARC: UP10000173CC9; UNIPARC: UP100000173CC9; UNIPARC: UP100000173CC9; UNIPARC: UP10000173CC9; UNIPARC: UP10000173CC9; UNIPARC:
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IIIa <DO3A>
laminin-type E
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hypothetical protein T21D9.2 - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Species: T5-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C,Accession: T29774
R;Mhan, M.; Hawkins, J.
R;Mhan, M.;Mhan, M.;M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83 KKGYRCTTEAEQDIEEEKVEKIE-LNDSVNENSDTVGQIVHYIMKNEANAD-----VL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               135 KAMVADNSLYDPESPVTPSTPGSPPV----SPGPLSPGGTPGKHVCGHHLHTVGGVVER 189
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P;916-1169/Product: 29K protein #status predicted <PRT>
P;1170-1857/Product: cylindrical inclusion protein #status predicted <CIP>
P;1139-1314/Region: nucleotide-binding motif A (P-loop)
P;1339-1314/Region: nucleotide-binding motif B
P;1319-1346/Region: DEXH motif
P;1819-1346/Region: DEXH motif
P;1819-2317/Product: nuclear inclusion protein a #status predicted <NIB>
P;2294-2811/Product: coat protein #status predicted <COP>
P;2812-3141/Product: coat protein #status predicted <COP>
P;1920/Binding site: phosphoryl-RNA (Tyr) (covalent) #status predicted
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Sequence 264, App
Sequence 521, App
Sequence 511, App
Sequence 314, App
Sequence 310, App
Sequence 326, Ap
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Sequence 1, Application US/09910562

Revent No. US20020098163A1

GENERAL INFORMATION:

TITLE OF INVENTION: Human Tumor Necrosis Factor Receptors TR21 and TR22

FILE REPRESENCE: PF930

CURRENT APPLICATION NUMBER: US/09/910,562

CURRENT PILING DATE: 2001-07-23

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 2000-07-27

PRIOR FILING DATE: 2000-07-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Version 3.0

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Matches 1291; Conservative
        TYPE: DNA ORGANISM: homo sapiens
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GENERAL INFORMATION:

APPLICANT: Sergy, Ze et al.

TITLE OF INVENTION: Human Tumor Necrosis Factor receptors TR21 and TR22

FILE REFERENCE: PF530C1

CURRENT APPLICATION NUMBER: US/10/620,562

CURRENT APPLICATION NUMBER: 09/910,562

PRIOR APPLICATION NUMBER: 09/910,562

PRIOR PILING DATE: 2001-07-23

PRIOR PILING DATE: 2000-07-24

PRIOR PELING DATE: 2000-07-24

PRIOR PELING DATE: 2000-07-24

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Version 3:1

SEQ ID NO 1
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RESULT 2 US-10-620-562-1 ; Sequence 1, Application US/10620562 ; Publication No. US20050090436A1

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; PRIOR PILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,89 ; PRIOR PILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,88 ; PRIOR PILING DATE: 1997-06-06 ; PRIOR PILING DATE: 1997-06-06			; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,89: ; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,90:	; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,90: ; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,895	; PRIOR FILING DATE: 1997-06-06; PRIOR APPLICATION NUMBER: 60/048,919; PRIOR FILING DATE: 1997-06-06; PRIOR APPLICATION NUMBER: 60/049,019	; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,97(; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,97;	; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,910 ; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/049,373	; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION UNDBER: 60/048,87: ; PRIOR APPLICATION NUMBER: 60/049,37.	; PRIOR FILING DATE: 1997-06-06 ; PRIOR APPLICATION NUMBER: 60/048,91	; FKIOK FILING DATE: 1997-06-06; PRIOR APPLICATION NUMBER: 60/048,94; PRIOR FILING DATE: 1997-06-06	; PRIOR APPLICATION NUMBER: 60/048,974; PRIOR FILING DATE: 1997-06-06; PRIOR APPLICATION NUMBER: 60/048,88;	PRIOR FILING DATE: 1997-06-06 PRIOR APPLICATION UNBER: 60/048,89	PRIOR APPLICATION NUMBER: 60/048,890 ; PRIOR FILING DATE: 1997-06-06	; PRIOR APPLICATION NUMBER: 60/048,96; PRIOR FILING DATE: 1997-06-06	; PRIOR APPLICATION NUMBER: 60/048,96; PRIOR FILING DATE: 1997-06-06 . DDIOD ADDITCATION NUMBER: 60/04 97:	FAICH PELICATION NUMBER: 00/040,00/ ; PRIOR FILING DATE: 1997-06-06 . DDIOD ADDITCATION NUMBER: 60/049 976	PRIOR FILING DATE: 1997-06-06 PRIOR APPLICATION NUMBER: 60/068.05-0	; PRIOR FILING DATE: 1997-12-18 ; PRIOR APPLICATION NUMBER: 60/068,064	; PRIOR FILING DATE: 1997-12-18 ; PRIOR PEPLICALION NUMBER: 60/068,05:	; FRIOR FILLING DAIE: 1997-12-18 ; PRIOR APPLICATION NUMBER: 60/070,923 . DDIOR PITING NAME: 1967-19-19		, PRIOR FILING DATE: 1998-01-30
	GGGCTGAAACCGTCAATGGGGAGGTGCCGGCAACACCTGTGAAGAGAGAG	901 CAGAGTAGCAGGTGAGCCGTGGTTTTGGTGACATTGGGGGCAGAGTGGTGCAGGGTGAGG 960 	961 AGAAGGTACTIGGAGCCTCCCAGGTGCTGTGGCAGCATAGGAATGGTATTIGACAGGGAA 1020 	1021 GIGGGAGAGCITICCTIGACCCAGGAAGACTGAGGGGGACTGAACATGATTACTTGTCTG 1080 	1081 CCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTCCAGGGGCTTGGCCTGTGTGA 1140 	1141 TAATGAGGATAGGGATTACTTGTGAGGCAATGTGGCATGGTGGGGATTGTGGCAACTA 1200 	1201 GAATTCACATCACCCACCATATAGGGCTTGCATTACCACGAGGCAGAAGCACCTAGTGT 1260 	1261 IGCTGCATCTTCTTACGCAAAAAAAAA 1291 	r. E	-09-933-767-56 Sequence 56, Application US/09933767	~	TITLE OF INVENTION: 207 Human Secreted Proteins FILE REFERENCE: PEOO/07P2 TITRENUT APPLICATION NUMBER: 115/09/033,767	CURRENT FILING DATE: 2001-08-22 PRIOR APPLICATION NUMBER: PCT/US01/05614	IOR FILING DATE: 2001-02-21 IOR APPLICATION NUMBER: 06/184,836	FKIOK FILING DATE: 2000-02-24 PRIOR APPLICATION VUMBER: 60/193,170 PRIOR FILING DATE: 2000-03-29	IOR PILING DATE: 1998-12-04	IOR APPLICATION NUMBER: PCT/US98/11422 IOR FILING DATE: 1998-06-04	IIOR APPLICATION NUMBER: 60/048,885	FALOK AFFILCATION NUMBEK: 60/049,3/5 PRIOR FILING DATE: 1997-06-06 BPRIOR ADDITICATION NUMBER: 60/048 89:	PRIOR FILING DATE: 1997-06-06 PRIOR APLICATION NUMBER: 60/048.880	7-06 ER: 7-06	
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PRIOR APPLICATION NUMBER: 60/073,164
PRIOR PILING DATE: 1998-01-30
PRIOR PILING DATE: 1998-05-18
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PRIOR APPLICATION NUMBER: 60/085,921
PRIOR PILING DATE: 1998-05-18
PRIOR PILING DATE: 1998-07-15
PRIOR PILING DATE: 1998-07-30
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NUMBER OF SEQ ID NOS: 1245
SOFTWARE: PLENTIN Ver: 2.0
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(CATLON: (328)
OTHER INFORMATION: n equals a,t,g, or
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CHER INFORMATION: n equals a,t,g, or US-09-933-767-56
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ORGANISM: Homo sapiens
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EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,971
EARLIER FILING DATE: 1997-06-06
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Publication No. US20030092893A1
GENERAL INFORMATION:
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Pred. No. 0;
5; Mismatches
; NAME/KEY: SITE
; LOCATION: (328)
; OTHER INFORMATION: n equals a,t,g, or c;
; NAME/KEY: SITE
; LOCATION: (336)
; OTHER INFORMATION: n equals a,t,g, or c;
; RAME/KEY: SITE
; LOCATION: (341)
; OTHER INFORMATION: n equals a,t,g, or c;
; RAME/KEY: SITE
; LOCATION: (341)
; OTHER INFORMATION: n equals a,t,g, or c;
; RAME/KEY: SITE
; LOCATION: (788)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-004-860-56
                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 97.9%;
Matches 1268; Conservative
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180 240 662 926 GCCCTGGGGGAGGGGGAAGCGACGCGGCGATGGCTCCGCGGGCACTCCCGGGGTCCG 184 ACAATGGGAGCAGCAGCACATTGCACTCCAGAACAGAGACGACCCCGTCGCCCAGCAACG 243 244 ATACTGGGAATGGACACCCAGAATATAGCATACGCGCTTGTCCCTGTGTTTTTTTCA 303 536 543 296 959 716 776 782 836 842 896 GCCCTGGGGGGGGGGGGAA-CGACGCGGGGATGGCTCCGCGGGCACTCCCGGGGTCCG 123 241 ATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTCTTTATCA 300 TGGGTCTCTTTGGCGTCCTCATTTGCCACCTGC---TTAAGAAGAAAGGCTATCGTTGTA 357 CAACAGAAGCAGAGCAAGATATCGAAGAGG-AAAAGGTTGAAAAGATAGAATTGAATGAC 416 CAACAGAAGCAGAGCAAGATATCGAAGAAGAAAAAGGTTGAAAAGWTAGRATTGAATGAC 423 AGTGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATGAAAAATGAA 476 424 AGTGTGAATGAAACAGTGACACTGTTGGGCAAATCGTCCACTACATGAAAATGAAAATGAA 483 602 AGGBATGTGTCTCATCGGTGTGAGGCACAAGCGGTGGCACTTTATAAAAGCCCACTAACAAG 722 902 9 64 CCGTCCTAGCCGCTGCTGTCTTCGTGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG 181 ACAATGGGAGCAGCGCGCACATTGCACTCCAGAACAGAGACGACCCCGTCGCCCAGCAACG 603 GGAACGCCAGGAAACACGTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTWGTCGAG GGCACAGAGTAGCAGGTGAGCCGTGGTTTTGGTGACATTGGGGGCCAGAGTGGTGCAGGT CCCGTGACCCCCAGCACAGGGAGCCCGCCAGTGAGTCCTGGGCCTTTGTCACCAGGG 544 CCCGTGACCCCCAGCACACCAGGAGCCCGCCAGTGAGTCCTGGG-CTTTGTCACCAGGG 1 CCCACGCGTCCGGCCCGCCCGCTCCGGAGCGCTCTGCCTTCCCGAGCGCGCGGACGCGCGC 597 GGGACGCCAGGGAAGCACGTCTGTGCCATCATCTGCATACGGTGGCCGGTGTTGTCGAG 657 AGGGATGTGTCATCGGTGTAGGCACAAGCGGTGGCACTTTATAAAGCCCACTAACAAG TCCAGAGAGAGCCACGGCGCCAAGGCGAGGTCACGGTCCTTTCTGTTGGCAGATTT 777 AGAGTTACAAAAGTGGAGCACAAGTCAAACCAGAAGGAACGGAGAAGCCTGATGTCTGTT AGAGTNACAAAAGTGGAGCACAAGTCAAACCAGAAGGAAGGAAGCCTGATGTCTGTT Gaps DB 5; Length 1603; ٠. د Indels 13; Query Match 92.7%; Score 1196.6; Best Local Similarity 97.9%; Pred. No. 0; Matches 1268; Conservative 5; Mismatches υ U GTHER INFORMATION: n equals a,t,g, or provided by the process of t 7 61 65 121 301 358 364 417 537 663 717 723 783 897 요 셤 셤 셤 셤 셤 ઠે ò 8 ð δ 셤 8 셤 ઠ g ð Š 셤 Š 요 Š ઠે 셤 ò g ò g à g 8

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Sequence 5597, Application US/10363345A
Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFRENCE: E01/1227
CURRENT PILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 5597
LENGTH: 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       246 CGTCGGTTTCCGAGCGGTTTTGTTTTTCGAGCGCGGAGGCGCGTTTTGCGGGAGGAG 305
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FRATURE:
CTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens);
CTHER INFORMATION: CpG-island No: 5597
US-10-363-345A-5597
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FOTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 5598
US-10-363-345A-5598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 8.9%; Score 115.4; DB 8; Length Best Local Similarity 81.2%; Pred. No. 6.4e-24; Matches 134; Conservative 0; Mismatches 31; Indels
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8.9%; Score 115.4; DB 8;
Best Local Similarity 81.2%; Pred. No. 6.4e-24;
Matches 134; Conservative 0; Mismatches 31;
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ORGANISM: Artificial Sequence
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US-10-363-345A-5598/c
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                                                             1017 GGAAGTGGGAAGCTTTCCTTGACCCAGGAAGACTGAGGGGGACTGAACATGATTACTTG 1076
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GGCACAGAGTAGCAGGTGAGCCGTGGTTTTTGGTGACATTGGGGGGCAGAGTGGTGCAGGGT
                                                                                                                                                 1023 GGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGACTGAACATGATTACTTG
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US 60/255,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR FILING DATE: 2000-10-24

PRIOR FILING DATE: 2000-11-20

PRIOR FILING DATE: 2000-11-30

PRIOR FILING DATE: 2000-11-16

PRIOR PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PRIOR DATE: 2001-01-16

PRIOR PRIOR DATE: 2001-01-16

PRIOR PRIOR DATE: 2001-01-6

PRIOR PRIUNG DATE: 2001-01-6

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PRIUNG DATE: 2001-01-6

PRIOR PRIUNG DATE: 2001-01-6

PRIOR PRIUNG DATE: 2001-05-09

SROID NOS: 957086

SROID NO 84619
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                                                                                                                             449 CGTCGGTTTCGGAGCGGTTTTGTTTTTTCGAGCGCGGACGCCGTTTTGGGGGAGGAG 390
                                                                              76 GGCGAAGCGACGCGCGCGATGGCTCCGCGGCACTCCCGGGGGTCCGCCGTCTAGCCGCTG 135
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APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
APPLICANT: Christian Piepenbrock
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: illnesses
TITLE OF INVENTION: illnesses
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT PILING DATE: 2003-03-03
SEQ ID NOS: 40712
LENGTH: 694
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Publication No. US20050064401A1

GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses or predisposition to certain
TITLE OF INVENTION: Diagnosis of illnesses
FILE REFERENCE: 82011
CURRENT APPLICATION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NOS: 40712
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
OTHER INFORMATION: CpG-island No: 5598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens); OTHER INFORMATION: CpG-island No: 5597
US-10-363-483A-5597
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8.9%; Score 115.4; DB 9; Length 694;
Best Local Similarity 81.2%; Pred. No. 6.4e-24;
Matches 134; Conservative 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                   136 CTGTCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG 180
                                                                                                                                                                                                                                                                                              329 TTGTTTTCGTGGGGGCGTCGTCGTCGTCGTCGTGGTTTCGG 285
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US-10-363-483A-5597
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Sequence 5599, Application US/10363345A

Publication No. US20040234960A1

GENERAL INFORMATION:
APPLICANT: Alexander olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Wethod for determining the degree of methylation of defined
TITLE OF INVENTION: Cytosines in genomic DNA in the sequence context of 5'-CpG-3
FILE REFERENCE: E01/1227
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NOS: 40712
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Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
TITLE OF INVENTION: Method for determining the degree of methylation of defined
TITLE OF INVENTION: Cycosines in genomic DNA in the sequence context of 5'-CpG-3; FILE REFERENCE: E01/1227
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                                                                                                                                                                                                                                                                                                    389 GGCGAAGCGACGCGCGATGGTTTCGCGGGTTTTTCGGGGGTTCGTCGTTTTAGTCGTTG 330
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OTHER INFORMATION: Chemically treated genomic DNA (Homo sapiens):
OTHER INFORMATION: CpG-island No: 5599
US-10-363-345A-5599
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         Length 694;
                                                                                                                                                                                                                                                                                                                                                                                            329 TIGITITICGIGGGAGGCGTCGTGAGTTCGTCGTTGGTGGTTTTCGG 285
                                                                                                                                                                                                                                                                                                                                                              136 CTGTCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG 180
      Score 115.4; DB 9; Length Pred. No. 6.4e-24; 0; Mismatches 31; Indels
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         8.9%;
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Query Match
Best Local Similarity 81.2*
Matches 134; Conservative
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Publication No. US20050064401A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Alexander Olek
APPLICANT: Kurt Berlin
TITLE OF INVENTION: illnesses
FILE REFERENCE: 82011
CURRENT APPLICANTION NUMBER: US/10/363,483A
CURRENT FILING DATE: 2003-03-03
NUMBER OP SEQ ID NOS: 40712
SEQ ID NO 5599
LENGTH: 694
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US-10-363-483A-5599
                                                                                                                                                              OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) OTHER INFORMATION: CpG-island No: 5600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 8.1%; Score 104.6; DB 9; Length 694; Best Local Similarity 73.2%; Pred. No. 1.2e-20; Matches 134; Conservative 0; Mismatches 49; Indels 0;
                                                                                                                                                                                                                                        Query Match 8.1%; Score 104.6; DB B; Length 694; Best Local Similarity 73.2%; Pred. No. 1.2e-20; Matches 134; Conservative 0; Mismatches 49; Indels 0
CURRENT APPLICATION NUMBER: US/10/363,345A CURRENT FILING DATE: 2003-03-03 NUMBER OF SEQ ID NOS: 40712 SEQ ID NO 5600 LENGTH: 694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
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5. W. S. C.

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Sequence 5600, Application US/10363483A;
Sequence 5600, Application US/10363483A;
Publication No. US20050664401A1
GENERAL INFORMATION:
APPLICAMT: Abrander Olek
APPLICAMT: Christian Piepenbrock
APPLICAMT: Christian Piepenbrock
APPLICAMT: Kurt Berlin
TITLE OF INVENTION: Diagnosis of illnesses
TITLE OF INVENTION: illnesses
FILE REPERENCE: 82011
CURRENT PILING DATE: 2003-03.
CURRENT PILING DATE: 2003-03.
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 5600
LENGTH: 694
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Publication No. US20050228172A9

GENERAL INPORMATION:
I APPLICAMY: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: NUCLECTION OF STATE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens); OTHER INFORMATION: CpG-island No: 5600
US-10-363-483A-5600
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Matches 134; Conservative
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SEQ ID NO 2551
LENGTH: 2205
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-2551
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0; Gaps Query Match 5.7%; Score 74; DB 4; Length 2205; Best Local Similarity 100.0%; Pred. No. 4.4e-11; Matches 74; Conservative 0; Mismatches 0; Indel8 ઠે

464 CATGAAAATGAAG 477 ||||||||||||| 219 CATGAAAATGAAG 232

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Search completed: February 23, 2006, 17:25:18 Job time : 1205 secs

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Sequence 84619, A Sequence 2551, Ap Sequence 2553, Ap Sequence 2553, Ap Sequence 720502, Sequence 720503, Sequence 720505, Sequence 3, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 1133, Ap Sequence 1133, Ap Sequence 1133, Ap Sequence 3, Appli Sequence 133, Appli Sequence 3, Appli Sequence 28155, A Sequence 184526, Sequence 18356, A Sequence 18356, A Sequence 28355, A Sequence 2
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2: /cgn2_6/ptodata/1/pubpn3/USOB NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpn3/USOT NEW PUB.seq:*
4: /cgn2_6/ptodata/1/pubpn3/USOT NEW PUB.seq:*
5: /cgn2_6/ptodata/1/pubpn3/USOF NEW PUB.seq:*
6: /cgn2_6/ptodata/1/pubpn3/USOF NEW PUB.seq:*
7: /cgn2_6/ptodata/1/pubpn3/USOF NEW PUB.seq:*
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11: /cgn2_6/ptodata/1/pubpn3/USOF NEW PUB.seq:*
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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US-09-925-065A-2551
US-09-925-065A-2552
US-09-925-065A-2553
US-09-925-065A-720502
US-09-925-065A-720504
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US-09-925-065A-720504
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Maximum Match 100%
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. Pebl	ication N	O. US20 MATION:	0401810	48A1			
,	LICANT: W	ang, Da	ivid G.	;	:		
	TITLE OF INVENTION: Identification of INVENTION: Nucleotide	ENTION:	Nucle	rıca otid	ition and Mapping of Single le Polymorphisms in the Human (an Genome	
	E REFEREN	CB: 108	1827.135 INTERPRED	. 119/09	00 / 00 / 00 / 00 / 00 / 00 / 00 / 00		
	CURRENT FILING DATE:	NG DATE	2001-08	-98	000000000000000000000000000000000000000		
	OR APPLICATION NUMBER: US 60	ATION N	TUMBER:	us e	60/243,096		
	OR APPLIC	ATION N	TOMBER:	9 SN	60/252,147		
	PRIOR FILING	DATE	2000-11	-20			
	OR APPLIC	ATION N	OMBER: 2000	9 67-	60/250,092		
	OR APPLIC	ATION N	TUMBER:	us 6	0/261,766		
	OR FILING	DATE:	2001-01	-16			
	OR APPLIC	ATION A	UMBER:	200	0/289,846		
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SEO	O ID NO 846 LENGTH: 591	19					
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GENERAL INFUGUATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome FILE REFERENCE: 108627.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT PILING DATE: 2001-08-08

PRIOR PILING DATE: 2001-024

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-20

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/251,766

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-11-6

PRIOR PILING DATE: 2001-11-6

PRIOR PILING DATE: 2001-11-6

PRIOR PILING DATE: 2001-01-6

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16
                                                                                                          355 GTACAACAGAAGCAGAGCAAGATATCGAAGAAAAGGTTGAAAAGATAG 405
                                                                                                                                                     291 GTACAACAGAAGCAGAGGAAATATCGAAGAAGGAAAAGGTTGAAAAGATAG 341
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100.0%; Pred. No. 2.9e-10;
ive 0; Mismatches 0; Indels
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Publication No. US20040181048A1
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Matches 74; Conservative
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ORGANISM: Homo sapiens
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159 AGAATTGAATGACAGTGTGAATGAAAAACAGTGACACTGTTGGGCAAATCGTCCACTACAT 218
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| Publication No. US20040181048A1
| GENERAL INFORMATION:
| APPLICANT: Wang, David G. |
| TITLE OF INVENTION: Identification and Mapping of Single |
| TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome |
| FILE REPERENCE: 108827.135 |
| CURRENT APPLICATION NUMBER: US/09/925,065A |
| CURRENT APPLICATION NUMBER: US 60/243,096 |
| PRIOR APPLICATION NUMBER: US 60/25,147 |
| PRIOR APPLICATION NUMBER: US 60/25,147 |
| PRIOR APPLICATION NUMBER: US 60/250,092 |
| PRIOR PILING DATE: 2000-11-20 |
| PRIOR PILING DATE: 2001-01-30 |
| PRIOR PILING DATE: 2001-01-30 |
| PRIOR PILING DATE: 2001-01-6 |
| PRIOR APPLICATION NUMBER: US 60/261,766 |
| PRIOR PILING DATE: 2001-01-6 |
| PRIOR PILING DATE: 2001-01-6 |
| PRIOR APPLICATION NUMBER: US 60/289,846 |
| PRIOR PILING DATE: 2001-01-6 |
| PRIOR APPLICATION NUMBER: US 60/289,846 |
| PRIOR APPLICATION NUMBER: US 60/289,8
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Publication No. US20040181048A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT APPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
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                                                                                                                                                                                                                                     Length 2205;
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5.7%; Score 74; DB 6; Le
Best Local Similarity 100.0%; Pred. No. 2.9e-10;
Matches 74; Conservative 0; Mismatches 0;
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2.9e-10;
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LENGTH: 2205
TYPE: DNA
ORGANISM: Homo sapiens
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US-09-925-065A-2553
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US-09-925-065A-2552
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Fublication No. US20040181048A1
GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: UNCLEOCIDE POLYMOLPHISMS in the Human Genome
FILE REPERENCE: 10887.135
CURRENT APPLICATION NUMBER: US 60/243,096
FRIOR FILING DATE: 2000-10-24
FRIOR FILING DATE: 2000-11-20
FRIOR APPLICATION NUMBER: US 60/250,092
FRIOR APPLICATION NUMBER: US 60/261,766
FRIOR APPL
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PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PLING DATE: 2000-11-30
PRIOR PLING DATE: 2001-11-30
PRIOR PLING DATE: 2001-16
PRIOR PLING DATE: 2001-01-16
PRIOR PILING DATE: 2001-01-16
PRIOR PRIOR PRIOR DATE: 2001-01-16
SPIOR PILING DATE: 2001-01-16
PRIOR PRIOR PRIOR DATE: 2001-05-09
SOUTHARE: PASTESQ for Windows Version 4.0
SSOTTWARE: PASTESQ for Windows Version 4.0
ENGTH: 2480
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US-09-925-065A-720502
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US-09-925-065A-720503
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US-09-925-065A-720503
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404 AGAATTGAATGACAGTGTGAAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACAT
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GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITIE OF INVENTION: Identification and Mapping of Single

TITIE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 100827.135

CURRENT APPLICATION NUMBER: US 60/25,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/25,147

PRIOR APPLICATION NUMBER: US 60/250,092

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2000-11-30

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846

PRIOR PILING DATE: 2001-01-16

PRIO
                                                                                                                 GENERAL INFURCATION:

GENERAL INFURCATION:

TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
TITLE OF INVENTION: Nuclectide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A

CURRENT APPLICATION NUMBER: US 60/243,096

PRIOR PILING DATE: 2000-10-24

PRIOR PILING DATE: 2000-11-24

PRIOR PILING DATE: 2000-11-24

PRIOR PILING DATE: 2000-11-16

PRIOR APPLICATION NUMBER: US 60/261,766

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FRESCE for Windows Version 4.0

SEC ID NO 720504
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100.0%; Pred. No. 3e-10;
tive 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 3e-10;
Matches 74; Conservative 0; Mismatches 0; Indels
Sequence 720504, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
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Best Local Similarity 100..
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; ORGANISM: Homo sapiens
US-09-925-065A-720504
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ORGANISM: Homo sapiens
US-09-925-065A-720505
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RESULT 7 US-09-925-065A-720504

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                                                        434 AGAATTGAATGACAGTGTGAATGAAAACAGTGACACTGTTGGGGCAAATCGTCCACTACAT 493
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404 AGAATTGAATGACAGTGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACAT 463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            692 ciccarcerciciririris cercardad de contra d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                872 cerecrecerrearcacadadadadadadadadecreceseceredadegecrecrea 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1, Application US/11042814

Publication No. US20060024267A1

Sequence 1, Application S. US20060024267A1

SERRAL INFORMATION:

APPLICANT: Jung, Shuqian

APPLICANT: Welcher, Andrew A

APPLICANT: Boedigheimer, Michael J

APPLICANT: Shu, Junyan

APPLICANT: Gary M. Foo.

TITLE OF INVENTION: TNFr/OPG-LIKE MOLECULES AND USES THEREOF

FILE REFERENCE: 01017/36654

CURRENT APPLICATION NUMBER: US/11/042,814

CURRENT FILING DATE: 2005-01-25

PRIOR PLING DATE: 2005-01-25

PRIOR APPLICATION NUMBER: US/99/724,037

PRIOR PLING DATE: 2000-11-28

NUMBER OF SEQ ID NOS: 28

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 2638
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Pred. No. 6.3e-06;
0; Mismatches 104; Indels 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 55.5%;
Matches 137; Conservative
                                                                                                                                                                                                                                                      464 CATGAAAATGAAG 477
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; LOCATION: (195)..(1484)
US-11-042-814-1
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 509 AGATAAC 515
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; Sequence 3, Application US/11042814; Publication No. US20060024267A1; GENERAL INFORMATION: APPLICANT: Welcher, Andrew A; APPLICANT: Boedigheimer, Michael J; APPLICANT: Shu, Junyan; APPLICANT: Shou, Junyan; APPLICANT: Gary M. Fox

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239 CGATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTTTAT 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            299 CATGGGTCTCTTTGGCGTCCTCATTTGCCACCTGCTTAAGAAGAAAGGCTATCGTTGTAC 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              753 TAGGACTIGAAGATGCCAACGAGGACACCATTGGAGTCCTGCTGCGCCCTGATCACAGAA 812
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TITLE OF INVENTION: TWF*/OPG-LIKE MOLECULES AND USES THEREOF FILE REFERENCE: 01017/36854
; CURRENT APPLICATION NUMBER: US/11/042,814
; CURRENT FILING DATE: 2005-01-25
; PRIOR APPLICATION NUMBER: US/10/146,574
; PRIOR APPLICATION NUMBER: US/10/146,574
; PRIOR PILING DATE: 2002-05-15
; PRIOR PILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PALENT VET. 2.0
; SEQ ID NO 3
; LENGTH: 2479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 3.9%; Score 50.6; DB 12; Length Best Local Similarity 51.6%; Pred. No. 0.001; Matches 144; Conservative 0; Mismatches 129; Indels
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; NAME/KEY: CDS
; LOCATION: (91)..(1398)
US-11-042-814-3
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CORGANISM: Homo sapiens
US-09-925-065A-38365
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AFPLICANT: Boldog, Ference
TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
FILE REFERENCE: 21402-251
CURRENT APPLICATION NUMBER: 0(0/262,892
REIOR APPLICATION NUMBER: 60/262,892
REIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-01-19
PRIOR PLING DATE: 2001-01-24
REIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-24
PRIOR PLING DATE: 2001-01-25
PRIOR APPLICATION NUMBER: 60/264,117
PRIOR PLING DATE: 2001-01-25
PRIOR PLING DATE: 2001-01-26
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PLING DATE: 2001-03-02
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
PRIOR PLING DATE: 2001-03-14
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SOFTWARE: Patentin Ver. 2.1
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Tchernev, Velizar
Zhong, Mei
Anderson, David
Ballinger, Robert
Gerlach, Valerie
Spytek, Kimberly
Ratelli, Luca
Kekuda, Ramesh
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Burgess, Cahterine
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Gusev, Vladimir
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Zerhusen, Bryan
Andrew, David
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Best Local Similarity 48.29
Matches 120; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vernet, Corine
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; LOCATION: (85)..(1143)
US-10-055-877-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pena, Carol
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TITLE OF INVENTION: COMPUTATIONAL METHOD FOR IDENTIFYING ADHESIN AND ADHESIN-LIKE
TITLE OF INVENTION: PROTEINS OF THERAPEUTIC POTENTIAL
FILE PEPELCATION OF THE SOFT AND ADHESIN-LIKE
FILE REPERENCE: 30853/40359A
CURRENT APPLICATION NUMBER: US/11/052,554A
CURRENT FILING DATE: 2005-02-07
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-20
PRIOR PILING DATE: 2004-07-30
PRIOR PILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 763
SOFTWARE: PATENTIN VERSION 3.3
SOFTWARE: PATENTIN VERSION 3.3
                                                                                                            1050 CTGAGGGGGACTGAACATGATTACTTGTCTGCCTAGAGCTTCTTGTAAAGAAGTCACAAA 1109
                                                                                                                                                                                                             1110 CT-TAGTGCCTCCAGGGGCTTGGCCTGTGTGATAATGAGGATAGAGGATTACTTGTGAGG 1168
                                                                                                                                                                                                                                                                                                               61 GCCCTGGGGGAAGGGGGACGACGCGATGGCTCCGCGGGCACTCCCGGGGGTCCG 120
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                                                                                                                                                                                                                                                          245 arcanarieccrecidededecadecaderacracrarragranacaderagrandade 304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  365 TGCCTCCTCCTCCATTTAATAGGTAGGCAGGTATATGGGCTAATCTTACCAGAA 417
     3.6%; Score 46.6; DB 6; Length 1155; ilarity 52.8%; Pred. No. 0.01; Conservative 0; Mismatches 109; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.5%; Score 45; DB 12; Length 1731;
llarity 53.0%; Pred. No. 0.033;
Conservative 0; Mismatches 85; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis H37Rv
US-11-052-554A-548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-11-052-554A-548/c

Sequence 548, Application US/11052554A

; Publication No. US20050288866Al

; GENERAL INFORMATION:
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Publication No. US20050288241A1
GENERAL INFORMATION:
APPLICANT: DeCristofaro, Marc
APPLICANT: Padigaru, Muralidhara
APPLICANT: Miller, Charles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 96; Conserva
                               Best Local Similarity
Matches 123; Conserv
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TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REPERBNCE: 108827,135
CURRENT FILING DATE: 2001-08-08
PRIOR PRICH PAPLICATION NUMBER: US 60/243,096
PRIOR PILING DATE: 2000-10-24
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-20
PRIOR PILING DATE: 2000-11-30
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56.6%; Pred. No. 0.22;
tive 0; Mismatches 59; Indels
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Sequence 2835, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT PILNG DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24

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GenCore version 5.1.7 Copyright (c) 1993 - 2006 Biocceleration Ltd. OM nucleic - nucleic search, using sw model Run on: February 23, 2006, 14:49:57; Search time 6919 Seconds (without alignments) 10606.286 Million cell updates/sec Title: US-10-620-562-1 Sequence: 1291 Scoring table: IDENTITY NUC Gapop 10.0, Gapext 1.0 Searched: 5883141 seqs, 28421725653 residues Total number of hits satisfying chosen parameters: 11766282 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Post-processing: Minimum Match 0* Maximum Match 100* Listing first 45 summaries	Database : GenEmbl:* 1: 9p ba:* 2: 9p in:* 3: 9p on:* 5: 9p on:* 5: 9p ph:* 6: 9p ph:* 7: 9p ph:* 11: 9p r:* 11: 9p r:* 12: 9p un:* 13: 9b un:* 14: 9p h:* 15: 9p h:* 15: 9p h:* 16: 9p h:* 17: 9p h:* 18: 9p h:* 18: 9p h:* 19: 9p h:*	77008882999999971 GT

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Mammalia; Butheria; Buarchontoglires; Primates; Catarrhini;
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YANGGU SHI, CHARLES FLORENCE, KIMBERLY FLORENCE, DAVID W LAFLEUR
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PING FAN,YING FEI WEI,CARRIE L FISCHER,DANIEL R SOPPET,YI L
ZHIZHEN ZENG,
HLA KYAW,GUO LIANG YU,PING PENG,PATRICK J DILLON,GREGORY A
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PC A01037/18,40104,C12Q1/00,C12Q1/02,C12Q1/68,C12N5/00
PC C12N15/06,C12N15/09,C12N15/10,C12N15/11,G01N33/53 CC
Strandedness: Double;
CT Topology: Linear:
FR FRY
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Pred. No. 1.8e-276;
5; Mismatches 13; Indels
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Best Local Similarity 97.9%;
Matches 1268; Conservative
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963 GAGGAGAAGGTACTTGGAGCCTCCCAGGTGCTGGCAGCATAGGAATGGTATTTGACAG 1022
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PI KOJI HAYASHI
PC
C12N15/09, C07K14/47, C07K16/18, C12N1/15, C12N1/19, C12N1/21, C12N5/ PC
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JP 200017376-A/90
22-JAN-2002
07-JUL-2000
JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
Homo sapiens
Eukaryota, hetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                            GGCACAGAGTAGCAGGTGAGCCGTGGTTTTGGTGACATTGGGGGCAGAGTGGTGGTGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                               1023 GGAAGTGGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGACTGAACATGATTACTTG
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                                                                                  TCCAGAGAGAGCAGACCACGCGCCAAGGCGAGGTCACGGTCCTTTCTGTTGGCAGATTT
                                                                                                                                                                                                                  957 GAGGAGAAGGTACTIGGAGCCICCCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGACAG
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 AGGGATGTGTGTCATCGGTGTAGGCACACAGGCGGTGGCACTTTATAAAGCCCACTAACAAG
                                                               TCCAGAGAGAGCAGACCACGGCGCCAAGGCGAGGTCACGGTCCTTTCTGTTGGCAGATTT
                                                                                                                                                                                               AGTGGGGCTGAAACCGTCAATGGGGAGGTGCCGGCAACACCCTGTGAAGAGAAGGAACGCAGT
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1 (bases 1 to 1320)
Ota,T., Isogai,T., Nishikawa,T., Kawai,Y., Sugiyama,T. and Hayashi,K.
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JP 2002017376-A/90.
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BD123581
LOCUS
DEFINITION
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VERSION
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SOURCE
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AUTHORS
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Young, P., Greene, J.M., Ferrie, A.M., Ruben, S.M., Rosen, C.A.,
Hu, J.S., Olsen, H.S., Ebner, R., Brewer, L.A., More, P.A., Shi, Y.,
Florence, C., Florence, K., LaFleur, D.W., Ni, J., Fan, P., Wei, Y.F.,
Fischer, C.L., Soppet, D.R., Li, Y., Zeng, Z., Kyaw, H., Yu, G.L.,
Frischer, C.L., Soppet, D.R., Li, Y., Zeng, Z., Kyaw, H., Yu, G.L.,
207 human secreted proteins
Patent: EP 1428833-A 56 16-JUN-2004;
Human Genome Sciences, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGTCCTAGCCGCTGCTGTCTTCGTGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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Hayashi,K.
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Patent: EP 1514933-A 179 16-MAR-2005;
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Toganisma-"Homo sapiens"
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    C12P21/02, C12Q1/68//C12P21/08, C12N15/00, C12N5/00
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99.4%; Pred. No. 3.2e-205;
ive 0; Mismatches 5; Indels
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Secretory protein or membrane protein
FH Key Location/Qualifiers
FT CDS (90). (902).
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/proteIn_id="CAC39770.1"
/bx xref="cut.14272664"
/translation="WAPRALPGESAVLAAAVFVGGAVSSPLVAPDNGSSRALHSRTETT
PSPSNDTGNGHPEYIAYALVPVPFIMGLPGVLICHLKKKGYRCTTEAEQDIEEEKVB
KIELNDSVNENSDTVGQIVHYTMKNENSADVLAEAMADNNSLYDPESPYTPSTPGSPPV
SPPGPLSPGGTPGKHVCGHHLHTVGGVVERDVCHRCRHKWHFIKPTKSPRRGF
EVTVLSVGRFRVTKVEHKSNQKERRSLAMSVSGAETVNGSVPATPVKRERSGFE"
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
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Hayashi,K.
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Patent: EP 1067182-A 179 10-JAN-2001;
Helix Research Institute (JP)
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PRI 09-JUL-2005 900 AK075468 1320 bp mRNA linear Homo sapiens cDNA PSEC0162 fis, clone PLACE1009772.

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Hominidae, Homo.

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Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,
Klausner, R.D., Collins, P.S., Wagner, L., Shemmen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Haieh, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S.,
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  TGTGTCATCGGTGTAGGCACAAGCGGTGGCACTTATAAAGCCCACTAACAAGTCCAGGG
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Ishii,S., Saito,K., Yamamoto,J., Wakamatsu,A., Nagai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.,
Nakamura,Y., Nagahari,K., Sugano,S. and Isogai,T.,
HRI human cDNA sequencing project
Unpublished
Is Jobass 1 to 1120)
Is Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (20-MAR-2002) Takao Isogai, Helix Research Institute,
Genomice Laboratory; 1332-3 Yana, Kisarazu, Chiba, 292-0812, Japan
Genomice Laboratory; 1332-3 Yana, Kisarazu, Chiba, 292-0812, Japan
(E-mail:genomics@hxi.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
HRI human cDNA sequencing project; cDNA 5- & 3'-end one pass
sequencing, clone selection and full insert sequencing: Helix
Research Institute (supported by Japan Key Technology Center etc.);
CDNA library construction: Institute of Medical Science, University
of Tokyo, Laboratory of Genome Structure, Human Genome Center.
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Pspsndtgnghpeytayalvpyffinglegvl.tchlkkkgyrctteaegdieeekve
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Spgplspegtpkkyvcghhlhtvggvyerdychkchkkmhetikpyrksresppre
Evtvlsvgrprtytkvehksnokerrslamsvsgaettvngevpatpykrersgte
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                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
Hominidae, Homo.
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/note="cloning vector: pME18SFL3"
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                    AK075468.1 GI:22761572
oligo capping; fis (full insert sequence).
Homo sapiens (human)
Homo sapiens
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/codon_start=1
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Matches 903; Conservative
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Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini,
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Hayashi,K.
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JP 2002017376-A/293.
Homo sapiens (human)
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.N.A.G.B. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web Site:
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 88 Row: n Column: 22.
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KIELNDSVNENSDTVGQIVHYIMKNEANADVLKAMVADNSLYDPESPVTPSTPGSPPV
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EVTVLSVGRFRVTKVEHKSNQKERRSLMSVSGAETVNGEVPATPVKRERSGTE"
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Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Mabramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J., Malek, J.A., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, B.J., Lu, X., Gibbs, R.A., Falton, E., Ketteman, M., Madan, A., Rodrigues, S., Sanchez, A., Whiting, M., Madan, A., Rodrigues, S., Bouffard, G.G., Blakesley, R.W., Touchman, J. W., Green, B.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.W., Sutterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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/tisue type="Panceas, Spleen, adult pooled"
/clone lib="NIH MGC_120"
/lab_host="DH10B"
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llarity 99.4%; Pred. No. 5.7e-205;
Conservative 0; Mismatches 5; Indels (
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGGGAGCAGCCGCACATTGCACTCCAGAACAAGACGACCCCGTCGCCCAGCAACGATA 243
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                                                                                                                                                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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 GTGTGTCATCCGGTGTAAGCACAANCGGTGGCACTTTATAAAGCCCCACTAACANGTCCAG
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Hayashi,K.
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llarity 98.3%; Pred. No. 1.2e-153;
Conservative 0; Mismatches 10;
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Patent: BP 1514933-4 466 16-MAR-2005;
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Sequence 466 from Patent EP1514933.
CS051580
                                                                                                                                                                                                                                                                                                                                                                                                             organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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              Homo sapiens (human)
JP 2002017376-A/293
22-JAN-2002
07-JUL-2000 JP 2000253173
TOSHIO OTA, TAKAO ISOGAI, TETSUO NISHIKAWA, YURI KAWAI, TOMOYASU SUGIYAMA,
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       ACCCCCAGCACACCAGGAGCCCGCCAGTGAGTCCTGGGCCTTTTGTCACCAGGGGGACG
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Secretory protein or membrane protein
                                                                                                                                                                                                                             'organism='Homo sapiens (human)'
                                                                                                                                                                                               Location/Qualifiers
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1. 726
Acrganism="Homo sapiens"
//organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
RESEARCH INSTITUTE
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	663 GTGTGTCAT-CGGTGGCACAACCGGTGGCACTTTATAAAGCCCACTAACAAGTCCAGG [REFERENCE 1 Adminidae; Homo. REFERENCE 1 AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W. TILLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof JOURNAL Patent: WO 020685798 + 13771 06-SEP-2002; PEATURES Location/Qualifiers Source 1.680	/mol_type="unassigned DNa" /db_xref="taxon:9606" ONEGIN Query Match 52.7%; Score 680; DB 6; Length 680; Best Local Similarity 100.0%; Pred. No. 2.2e-152; Matches 680; Conservative 0; Mismatches 0; Indels 0; Gaps 0; ATGGCTCGGGGGCTCGCGGGGTCGCCGTCTTGGTGGTGTTTTGTGGGGGG	
	RESULT 10 AX136544 LOCUS DOCUS DOCUS AX136544 AX13654 AX136544 AX13654 AX1365	Source	Db 1 ACT CONTINUED 1 ACT CONTINUED 1 ACT CONTINUED 1 ACT CONTINUED 2 ACT CONTINUED 3 ACT	

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAH31199.1"
db_xref="G1:21410499"
db_xref="G1:2140769"
db_xref="MG1:214076"
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GKHVCGHHLHTVGGVVERDVCQRCHKWHFIKPTNKTKEGRPRRQGEVTLSVGRFF
VTKVEHKSNQKERRSLMSVSGIESVNGDVPATPVKRERSDTE"
                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 58 Row: n Column: 7 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22122334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Mammary tumor. MMTV-LTR/INT3 model. 5 month old mouse. Taken by biopsy." /clone_lib="NCI_CGAP_Mam2"
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/codon_start=1
/product="expressed sequence AA536743"
                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 622.2; DB 9;
Pred. No. 1.9e-138;
0; Mismatches 173;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="GeneID:100532"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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Best Local Similarity 80.8%;
Matches 739; Conservative 0
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1 (bases 1 to 2581)

2 Strausberg, E.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shemmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haie, P., Stapleton, M., Soares, M.M. B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S. Carninci, P., Frange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Hale, S., Garcia, A.M., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodrigues, R.M., Butterfield, Y.S., Krzywinski, M.I., Salaska, U., Sanilus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A., Schein, J.B., Wann, J. Jones, S.J. and Marra, M.A., Schein, J. Butterfield analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC031198 2581 bp mRNA linear ROD 30-JUN-2004 Mus musculus expressed sequence AA536743, mRNA (cDNA clone MGC:37691 IMAGE:5059693), complete cds.
                                                                                         GTCCACTACATGAAAAATGAAGGAATGCTGATGTCTTAAAGGCGATGGTAGCAGAT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CATACGGTGGCGGTGTTGTCGAGAGGATGTGTGTCATCGGTGTAGGCACAAGCGGTGG 692
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CTTAAGAAGAAAGGCTATCGTTGTACAACAGAAGCAGAGCAGAGATATCGAAGAGGAAAAG 300
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                                                                                                                                                                                                                                                                                                                                            AACAGCCTGTATGATCCTGAAAGCCCCGTGACCCCCAGCACACCCAGGCCCCGCCAGTG 480
                                                                                                                                                                                                                                                                                                                                                                                                  AGTCCTGGGCCTTTGTCACCAGGGGACGCCAGGGAAGCACGTCTGTGGCCATCATCTG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGTCCTGGGCCTTTGTCACCAGGGGGGCCCAGGGAAGCACGTCTGTGGCCATCATCTG 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATACGGTGGCGGTGTTGTCGAGAGGGATGTGTGTCATCGGTGTAGGCACAAGCGGTGG 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CACTTTATAAAGCCCACTAACAAGTCCAGAGAGAGCAGACCACGGCGCCAAGGCGAGGTC 660
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Submitted (03-QN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACTITIATAAAGCCCACTAAACAAGTCCAGAGAAGAGCAGACCACGGCGCCAAGGCGAGGTC
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
SOURCE
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GKHVCGHILHTVGGVVERDVCQRCRHKRWHFIKPTNKTKEGRPRRQGEVTVLSVGRPR
VTKVEHKSNQKERRSLMSVSGIESVNGDVPATPVKRERSBTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Bmail: cgapbs-remail.nih.gov
Bmail: cgapbs-remail.nih.gov
CDNA Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NH: http://lgun.grc.nia.nih.gov/cDNA/)
EDNA Library Arrayed by: The I.M.A.G. CONSOrtium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site:
Contact: (Dickson, Mark) med@paxil.senford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             can be found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 TGCTGTCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGGACAATGGGAGCAG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73
                                                                                                                                                                                                                                                                                    Direct Submission

Submitted (03-FBB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC). Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be for
through IRA I.M.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 144 Row: a Column: 18.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="Embryo, whole, mouse, 7.5-dpc"
/clone lib="NIA Mouse 7.5-dpc Whole Embryo cDNA Library
(Long) "
   Smailus DE, Schnerch A, Schein JE, Jones SJ and Marra MA. Mammalian Gene Collection Program Team Generation and intital analysis of more than 15,000 full-length human and mouse CDNA sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGGCAGCCCTCGAGCTGCACCGTCTACCCCGGACCCCGGGAACGCCCGCGGGGCGGGGCGAGG
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                                                                                   numan and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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80.7%; Pred. No. 4.7e-138;
iive 0; Mismatches 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Mus musculus"
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/db_xref="GeneID:100532"
/db_xref="MGI:2140767"
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S Strausberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD, Collins FS, Wagner L, Shenmen CM, Schuler GD, Altechul SF, Zeeberg B, Buetow KH, Schaefer CF, Bheat NK, Hopkins RF, Jordan H, Moore T, Max SI, Wang J, Hsieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapheton M, Soares NB, Bonaldo MF, Casavant TL, Scheetz TB, Brownstein MJ, Uddin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bossk SA, McEwan PJ, McKernan KJ, Malek JA, Gunaranne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergen BJ, Lu X, Gibbs RA, Fahey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakeelley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U,
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sclurognathi, Muroidea, Muridae, Murinae, Mus
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Max SI, Wang J, Haieh F, Diatchenko L, Marusina K, Farmer AA, Rubin GM, Hong L, Stapleton M, Soares MB, Bonaldo MF, Casavant TL, Scheetz TE, Brownstein MJ, Usdin TB, Toshiyuki S, Carninci P, Prange C, Raha SS, Loquellano NA, Peters GJ, Abramson RD, Mullahy SJ, Bosak SA, McEwan PJ, McKernan KJ, Malek JA, Gunaratne PH, Richards S, Worley KC, Hale S, Garcia AM, Gay LJ, Hulyk SW, Villalon DK, Muzny DM, Sodergen BJ, Lu X, Gibbs RA, Fahrey J, Helton E, Ketteman M, Madan A, Rodrigues S, Sanchez A, Whiting M, Madan A, Young AC, Shevchenko Y, Bouffard GG, Blakesley RW, Touchman JW, Green ED, Dickson MC, Rodriguez AC, Grimwood J, Schmutz J, Myers RM, Butterfield YS, Krzywinski MI, Skalska U, Smallus DB, Schnerch A, Schein JB, Jones SJ and Marra MA.

Mammalian Gene Collection Program Team
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: MGC help desk
Email: cgapbe-remail.nih.gov
Tissue Procurement: Minoru Ko
CobNa Library Preparation: Yulan Piao and Minoru Ko (National
Institute on Aging, NIH: http://lgsun.grc.nia.nih.gov/cbNa/)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www.shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
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GKHVGHHIATVGGVVERDVCQRCHKRWHFIKPTKKTKEGRPRRQGEVTVLSVGRFR
VTKVEHKSNQKERRSLMSVSGIESVNGDVPATPVKRERSDTE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 144 Row: a Column: 19
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 22122334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Director MGC Project.

Direct Submission
Submitted (03-FRB-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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/clone="WGC:76510 INAGE:30012671"
/tissue type="Embryo, whole, mouse, 7.5-dpc"
/clone_lib="WIA Mouse 7.5-dpc Whole Embryo cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
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/mol_type="mRNA"
/strain="C57BL/6J"
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/note="Vector: pSPORT1"
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Stanusberg RL, Feingold EA, Grouse LH, Derge JG, Klausner RD,
Collins FS, Wagner L, Shenmen CM, Schuler GD, Altschul SF, Zeeberg
B, Buetow KH, Schaefer CF, Bhat NK, Hopkins RF, Jordan H, Moore T,
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Mammalia, Butheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
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  Length 2481;
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Score 620.6; DB 9;
Pred. No. 4.7e-138;
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MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. Mapping information for Genetics, Washington University, St. MCPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                    SOURCE INFORMATION:
restriction digest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VECTOR: pBACe3.6
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RESULT 15 AC027607/c LOCUS

AC027607 161070 bp DNA linear PRI 03-J Homo sapiens BAC clone RP11-36B15 from 4, complete sequence.

PRI 03-JUL-2002

GI:21686941 AC027607 AC027607.7 ACCESSION VERSION KEYWORDS SOURCE ORGANISM

Homo sapiens (human)

Homo sapiens Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Euarchontoglires, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 161070) Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) REFERENCE AUTHORS TITLE JOURNAL

2 (bases 1 to 161070) Cordas, M., Cotton, M., Bradshaw-Cordum, H. and Boyer, E. The sequence of Homo sapiens BAC clone RP11-36B15 Unpublished (2001)

PUBMED PUBMED AUTHORS TITLE JOURNAL REFERENCE AUTHORS TITLE JOURNAL

(bases 1 to 161070) Waterston, R.H. Direct Submission

Submitted (30-MAR-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 161070)

Waterston, R. REFERENCE AUTHORS TITLE JOURNAL

Direct Submission
Submitted (03-JUL-2002) Department of Genetics, Washington
Submitted (03-JUL-2002) Department of Genetics, Wissouri 63108,
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108,
On Jul 3, 2002 this sequence version replaced gi:15321552.
Genome Center

USA

Center: Washington University Genome Sequencing Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapienseten.wustl.edu
------ Summary Statistics
Center project name: H_NH0036B15

entire insert of this NOTICE: This sequence may not represent the entire insert of this colone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats, all regions were covered by sequence from more than one subclone; and the assembly was confirmed by

Louis

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org

The clone sequenced to the left is RP11-562N2, 2000 bp overlap; the clone sequenced to the right is RP11-9D8, 2000 bp overlap. Actual start of this clone is at base position 1 of RP11-36B15; actual end is at base position 161070 of RP11-36B15.

A transposon was identified in the vector portion of the clone. There is an unresolved tandem repeat from base 71075 to 71587.

Location/Qualifiers
1. .161070
/organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606" 2440. 2540 /rpt_family="MER1_type" /rpt_family="MER1_type" /rpt_family="Alu" 3189. 3251 /rpt_family="(TA)n" /rpt_family="Alu" /rpt_family="Alu" 1374 . 13969 1574 . 13969 1571 . 13969 1571 . 13870 1622 . 15870 1622 . 15870 1627 . 1597 1627 . 1597 1707 . 13180 1703 . 17180 1719 . 1754 1719 . 1754 7980. .9503 /rpt_family="L1" 9624. .9960 /rpt_family="MalR" 10113. .10602 /rpt_family="MalR" 10847. .10868 /rpt_family="(GGGAA)n" 12489. .13469 2489. .13469 rpt_family="MER2_type" 3470. .13773 rpt_family="Alu" /clone="RP11-36B15" /clone_lib="RPCI-11" 160. .301 /rpt_family="MaLR" 577. .942 repeat_region FEATURES

/rpt_family="MIR" repeat_region 2179121979 /rpt_family="MIR" repeat_region 2256822730 /rpt_family="MRIL" repeat_region 2374323902 /rpt_family="MRIL" repeat_region 2374323902 /rpt_family="MIR" repeat_region 2391223991 repeat_region 2400024024	region	arity onservat CCGTTGG ICCCCCT ICCCCCGI AGCCTGAI AGCCTGAI
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Aav84456 Human sec
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Ab4550 Human sec
Ad53833 Human cDN
Ad593174 Human cDN
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Ad121815 Novel hum
Aab98631 Human EST
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                                                                                                                               The present invention relates to novel human tumour necrosis factor (TNF) receptors, TR21 and TR22 and polynucleotides encoding them. Sequences of the invention are useful in the diagnosis, treatment and prevention of cancers (e.g., cancers of the adrenal gland, bone, urogenital or bone marrow, in particular breast and ovarian cancer), immune disorders (e.g., autoimmune haemolytic anaemia, rheumatoid arthritis, allergies, Addison's disease, ulcerative colitis), cardiovascular disorders (e.g., myocardial ischaemias), wound healing, neurological diseases (e.g., crebral anoxia, epilepsy) and infections diseases such as viral, bacterial, fungal and parasitic infections. They are also useful in gene therapy. The present sequence is a cDNA encoding human TR21 protein
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                                                   Two novel proteins, TR21 and TR22, which are members of the tumor necrosis factor receptor, useful for the diagnosis and treatment of immune disorders, cancer, cardiovascular disorders.
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DNA; 1603 (first entry) standard; 01-MAR-1999 AAV84456 RESULT

Human secreted protein gene 46 clone HCFMV39.

Human; secreted protein; fusion protein; gene therapy; protein therapy; diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia; developmental abnormality; foetal deficiency; blood; allergy; renal; ds; immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma; inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS; cognitive disorder; schizophrenia; proteate; obseivy; osteoclast; thyrus; costeoporosis; arthritis; testis; lung; thyroid; thyroid; disestion; endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm. 97US-0048875P Homo sapiens WO9854963-A2 06-JUN-1997; 04-JUN-1998; AAV84456

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The invention relates to nucleic acid sequences (AAV84411 to AAV84633)

cucoding human secreted proteins (AAW88534 to AAW88756). The secreted

cucoding human secreted proteins (AAW88534 to AAW88756). The secreted

cucoding pens sequences are deposited with the ATCC under deposit numbers

ATCC 97979, 97974, 97975, 97977, 209007, 209008, 209009, 209010,

cucoding comprising recombinant vectors containing the nucleic acid

sequences are used for the recombinant production of the secreted

cucoding comprising treating or ameliorating medical conditions e.g.

by protein or gene therapy. Pethological conditions e.g.

by protein or gene therapy. Pethological conditions e.g.

cucoding the presence of mutations in the new polynucleotides.

cucoding the presence of mutations in the new polynucleotides.

cucoding the presence of mutations in the new polynucleotides.

cucoding the diagnosis or treatment of cancer, neurodegenerative specific uses are described for each of the polynucleotides, based on confiscionates developmental abnormalities and focal deficiencies, blood disorders, tumours, leukemias, diseases and focal deficiencies, blood disorders, tumours, leukemias, diseases of the immune system, autoimmune diseases, hepatic and renal disease, lymphomas, inflammation, allergies, restenosis, prostate diseases, benchitis or malignancies, diseases of testes, lung cuch as osteoporosis, arthritis or malignancies, diseases of testes, lung partners. The present sequence represente and coloning a human secreted protein (see present sequence represente and clone identifying their binding partners. The present sequence represente and coloning a human secreted protein (see present sequence represente and clone identifying their binding partners. The present sequence represented and clone identification) 180 183 240 243 300 9 64 Ferrie AM, Ruben SM, Rosen CA, Hu J;
Brewer LA, Moore PA, Shi Y, Florence C;
DW, Mi J, Fan P, Wei Y, Fischer CL, Soppet DR;
H, Yu G, Feng P, Dillon PJ, Endress GA, 7 CCCACGCTCCGGCCCGCCGGCTCCGGAGCGCTCTGCCTTCCCGAGCGCGGGGA--CCGC ACAATGGGAGCGCGCACATTGCACTCCAGAACAGAGACGACCCCGTCGCCCCAGCAACG 241 ATACTOGGAATOGACACCCAGAATATTGCATACGCGCTTGTCCCTGTGTTCTTTATCA ATACTGGGAATGGACACCCAGAATATATTGCATACGGCCTTGTCCCTGTGTTCTTTATCA 191 ACAATGGGAGCAGCCGCACATTGCACTCCAGAACAGAGACGACCCCGTCGCCCAGCAACG CCCACGCGTCCGGCCCGCCGGCTCCGGAGCGGCTCTGCCTTCCCCGAGCGCGGGACGCGGGC New isolated human genes and the secreted polypeptides they encode useful for diagnosis and treatment of e.g. cancers, neurological disorders, immune diseases, inflammation or blood disorders. Similarity 97.9%; Score 1196.6; DB 2; Length 1603; Similarity 97.9%; Pred. No. 0; B; Conservative 5; Mismatches 13; Indels 9; Sequence 1603 BP; 416 A; 356 C; 449 G; 371 T; 0 U; 11 Other; Claim 4; Page 315-316; 772pp; English. Greene JM, Ferri Bbner R, Brewe: K, Lafleur DW, Young P, Greene JM, Ferri Olsen HS, Ebner R, Brewer Florence K, Lafleur DW, N Li Y, Zeng Z, Kyaw H, Yr Carter KC; Query Match Best Local Similarity 97.9 Matches 1268; Conservative WPI; 1999-059865/05. P-PSDB; AAW88579.

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Human secreted protein gene 46 SEQ ID NO:56.

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ABA83239

RESULT 3
ABA83239
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ABA83239 standard; cDNA; 1603

ABB50301 to ABB51287 and ABA83194 to ABA83441 represent human secreted proteins (I) and polynucleotide (II) sequences. (I) and (II) have various activities based on the tissues and cells the genes are expressed in.

Example of these activities include: immunomodulatory; antisclerotic; dermatological; immunosuppressive; antiinflammatory; immunostimulant; anti-angiogenic; optibalmological; cardiant; anti-angiogenic; optibalmological; neuroprotective; nootropic; anticonvulsant; antialzheimers; vascular; antiparkinsonian; antimicrobial; and vulnerary. (I) and (II) can be used in gene therapy and vaccine production. (I) and (II) can be used in the prevention, diagnosts and treatment of immune disorders (e.g. multiple calcrosis, systemic lupus erythematosus and human immunodeficiency virus (HIV) infections), hyperproliferative disorders (e.g. cancers and canchers diseases), cardiovascular diseases (e.g. Schintar syndrome, Chaga's cardiomyopathy and coronary arteriosclerosis), angiogenic disorders (e.g. corneal graft neovascularisation and disbetic calcorpathy), neurological disorders (e.g. Huntington's chorcea, Alzheimer's disease and Parkinson's disease), infectious diseases and/or for promocting wound healing, regeneration and/or chemotaxis. ABA83185 to ABA83193 and ABB50300 represent sequences used in the exemplification of Nucleic acids encoding 207 human secreted polypeptides, useful for preventing, diagnosing and/or treating, e.g. cancers, Parkinson's disease and diabetic retinopathy. Human; secreted protein; immunomodulatory; antisclerotic; anti-HIV; dermatological; immunosuppressive; antinflammatory; immunostimulant; orycestatic; cardant; vascular; anti-anglogenic; ophthalmological; neuroprotective; nootropic; anti-onvulsant; antialzheimens; vulnerary; antiparkinsonian; antimicrobial; gene therapy; vaccine; immune disorder; multiple sclerosis; systemic lupus erythematosus; HIV infection; cancer; human immunodeficiency virus; hyperproliferative disorder; wound healing; Gaucher's disease; cardiovascular disease; Scimitar syndrome; chemotaxis; corneal graft neovascularisation; diabetic retinopathy; regeneration; neurological disorder; Huntington's chorea; Alzheimer's disease; parkinson's disease; infectious disease; 88. P; Zeng Z; 9 64 CCCACGCGTCCGGCCCGCCGGCTCCGGAGCGGCTCTGCCTTCCCGAGCGCGGGACGCGGC CCACGCGTCCGGCCCGCCGGCTCCGGAGCGCTCTGCCTTCCCGAGCGCGGGGA--CCGC Gарв Ni J, Ebner R, Lafleur DW, Moore PA, Olsen HS, Rosen CA, tuben SW, Soppet DR, Young PE, Shi Y, Plorence KA, Wei Y; Plorence C, Hu J, Li Y, Kyaw H, Flacher CL, Ferrie AM, Fan Feng P, Endress GA, Dillon PJ, Carter KC, Brewer LA, Yu G, DB 4; Length 1603; 6 Sequence 1603 BP; 416 A; 356 C; 449 G; 371 T; 0 U; 11 Other; 13; Indels 92.7%; Score 1196.6; 97.9%; Pred. No. 0; 5; Mismatches Claim 1, Page 944-945; 1533pp; English. 21-FEB-2001; 2001WO-US005614. (HUMA-) HUMAN GENOME SCI INC. 29-MAR-2000; 2000US-0193170P. 24-FEB-2000; 2000US-0184836P. Best Local Similarity 97.9 Matches 1268; Conservative WPI; 2001-625724/72. P-PSDB; ABB50346. WO200162891-A2. Homo sapiens. 30-AUG-2001 Greene JM; н Query Match ઠ g 1256

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Human; ss; gene therapy; autoimmune disorder; multiple sclerosis; cancer; systemic lupus erythematosus; haematopoietic cell disorder; allergy; agammaglobulinaemia; ataxia telangiectasia; blood cosgulation disorder; afbrinogenaemia; thrombocytopenia; graft-versus-host disease; arthritis; inflammatory condition; ischaemia-reperfusion injury; infectious disease; hyperproliferative disorder; purpura; viral infection; regeneration; bacterial infection; ulcer; Alzheimer's disease; gene.
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DR; , Ruben SM, Rosen CA, Hu J; Moore PA, Shi Y, Florence C; Fan P, Wei Y, Fischer CL, Sopper Peng P, Dillon PJ, Endress GA; Young P, Greene JM, Ferrie AM, Olsen HS, Ebner R, Brewer LA, Florence K, Lafleur DW, Ni J, Li Y, Zeng Z, Kyaw H, Yu G, E Carter KC;

WPI; 2003-540804/51, P-PSDB; ABO44603.

New isolated protein, useful for preparing a composition for diagnosing or treating cancer, inflammatory, immune or infectious diseases.

Example 1; SEQ ID NO 56; 172pp; English.

The invention relates to an isolated HEWAE80 protein. The protein is useful for preparing a composition for diagnosing or treating autoimmune disorders e.g. multiple sclerosis and systemic lupus extrhematosus, haematopoietic cell disorders e.g. agammaglobulinaemia and ataxia telangiectsais; blood coagulation disorders e.g. afibrinogenaemia and thrombocytopenia; allergy; graft-versus-host disease; inflammatory conditions e.g. ischaemia-reperfusion injury and arthritis; hyperproliferative disorders e.g. cancer and purpura; infectious disease e.g. viral infection and bacterial infection. The polymucleotide or protein can be used to regenerate damaged tissue e.g. ulcers and Alzheimer's disease. The present sequence represents a novel human form part of the printed specification but was obtained in electronic format directly from USPTO at

240 120 180 300 AGTGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCATGAAAATGAA 476 957 GAGGAGAAGGTACTTGGAGCCTCCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGACAG 1016 123 183 243 303 416 536 836 896 GGCACAGAGTAGCAGGTGAGCCGTGGTTTTGGTGACATTGGGGGCAGAGTGGTGCAGGGT 956 357 363 423 543 596 602 656 662 716 722 776 782 842 902 GGCACAGAGTAGCAGGTGAGCCGTGGTTTTGGTGACATTGGGGGCAGAGTGGTGCAGGGT 962 9 64 CGTCCTAGCCGCTGCTGTGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG ATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTCTTATCA CAACAGAAGCAGGCAAGATATCGAAGAGG-AAAAGGTTGAAAAGATAGAATTGAATGAC ACAATGGGAGCGGCAGTTGCACTCCAGAACAGAGACGACCCCGTCGCCCAGCAACG TGGGTCTCTTTGGCGTCCTCATTTGCCACCTGC---TTAAGAAGAAAAAGGCTATCGTTGTA CCCGTGACCCCCAGCACACAGGAGCCCGCCAGTGACTCCTGGG - CTTTGTCACAGGG AGAGTTACAAAAGTGGAGCACAAGTCAAACCAGAAGGAACGGAGAAGCCTGATGTCTGTT CCACGCGCTCCGGCCCGCCGCCTCCGGAGCGGCTCTGCCTTCCCGAGCGGGGGA--CCGC GCCCTGGGGGAGGGGGAAGCGACGCGGCGATGGCTCCGCGGGCACTCCCGGGGTCCG CGGTCCTAGCCGCTGCTGTGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG 181 ACAATGGGAGCAGCCGCACATTGCACTCCAGAACAGAGACGACCCCGGTCGCCCAGCAACG ATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTCTTTATCA GGGACGCCAGGGAAGCACGTCTGTGGCCCATCATCTGCATACGGTGGGCGGTGTTGTCGAG CCCGTGACCCCCAGCACACAGGGGCCCGCCAGTGAGTCCTGGGCCTTTGTCACCAGGG TCCAGAGAGAGCAGACCACGCCCCAAGGCGAGGTCACCGGTCCTTTCTGTTGGCAGATTT TCCAGAGAGAGCAGACCACGGCGCCAAGGCGAGGTCCTTTCTGTTGCCAGATTT AGAGINACAAAAGIGGAGCACAAACCAGAAAGGAACGGAGAAGCCIGAIGIT 6 Length 1603; Sequence 1603 BP; 416 A; 356 C; 449 G; 371 T; 0 U; 11 Other; 13; Indels 9 segdata.uspto.gov/sequence.html?DocID=20030065160 80 Query Match 92.7%; Score 1196.6; Best Local Similarity 97.9%; Pred. No. 0; Matches 1268; Conservative 5; Mismatches ~ 61 65 121 124 184 241 244 301 304 358 364 417 124 484 537 544 597 657 663 717 723 777 783 837 843 477 603 897 ន្តដូនូ 셤 충 g 셤 Q 셤 ద a 원 셤 8 જે ò ਨੇ Š ઠે ò g 8 8 ò 셤 8 셤 ð 셤 ⋧ 셤 ઠે 셤 ò 용 ð

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1141
                                                                                                                                                                              ACTAGAATTCACATCACCACCATATAGGGCTTGCATTACCACGAGGCAGAAAGCACCTA 1256
                                                                                                                                                                                                                                         Human; ss; gene; secreted protein; precerebellin-like protein; neurodegenerative disorder; behavioural disorder; Alzheimer's disease; Parkinson's disease; schizophrenia; mania; dementia; paranoia; psychosis; autism; immune disorder; infection; inflammation; allergy; liver disorder; hepatoblastoma; jaundice; hepatitis; immunological disorder; AIDS; leukaemia; rheumatoid arthritis; sepsis; acne; psoriasis; cancer.
                                                               GGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGACTGAACATGATACTTG
                                                                                                     TCTGCCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTCCAGGGGCTTTGGCCTGT
                                                                                                                     TCTGCCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTCCAGGGGCTTGG-CTGT
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                                              GGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGGACTGAACATGATTACTTG
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PR 06-JUN-1997, 9718-0048971P.
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PR 06-JUN-1997, 9718-0049971P.
PR 06-JUN-1997, 9718-0049997.
PR 06-JUN-1997, 9718-004999.
PR 06-JUN-1998, 9718-004999.
PR 06-JUN-1998, 9718-
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ABO26522. The protein is encoded by one of 238 disclosed cDNA sequences encoding 238 secreted proteins. ABO26252 is a precerbellin-like protein. Also included are a composition composition composition and a carrier and an isolated protein produced by expressing the protein cited above by a cell, and recovering the protein. The proteins are useful for diagnosing or treating neurodegenerative and behavioural disorders (e.g. Alzheimer's disease, Parkinson's disease, Huntington's disease, schizophrenia, mania, dementia, paranoia, psychoses or autism), immune disorders (e.g. hapatoblastoma, infermmention, allergy), liver disorders (e.g. hapatoblastoma, infermantiol arthitis, sepais, and psorders (e.g. Alzheimer's rheumatoid arthitis, sepais, and, psorders (e.g. Alzkeimia, rheumatoid arthitis, sepais, and, psorders (e.g. Alzkeimia, sequence is one of the 238 disclosed cDNAs encoding a novel secreted sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at:- seqdata.uspto.gov/sequence.html?DocID=6525174B1
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Sequence 1603 BP; 416 A; 356 C; 449 G; 371 T; 0 U; 11 Other;

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GCCCTGGGGGGAGGGGGGACGCGATGGCTCCGCGGGCACTCCCGGGGTCCG 120
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                                                          CCCAGGGTCCGGCCGGCCGGGTCCGGAGCGCTTCCCGAGCGCGGGA--CCGC 64
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Score 1196.6; DB 9; Length
Pred. No. 0;
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 Query Match 92.7%;
Best Local Similarity 97.9%;
Matches 1268; Conservative
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1016 1076 1136 1196 1256 1022 1141 842 968 902 926 962 Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development. GAGGAGAAAGGTACTTGGAGCCTCCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGACAG GGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGGACTGAACATGATTACTTG AGTGGGGCTGAAACCGTCAATGGGGAGGTGCCGGCAACACCCTGTGAAGAGAGAAAGTG GAGGAGAAGGTACTTGGAGCCTCCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGACAG GGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGGACTGAACATGATTACTTG GTGATAATGAGGATAGAGGATTACTTGTGAGGCAATGTGGCCATGGTGGGGATTGTGGCCAA Grdataatigaggatagaggatractrorgaggcaatgregcatgeregggatrorgcaa ACTAGAATTCACATCACCACCACCATATAGGGCTTGCATTACCACGAGGGAGAAAGCACCTA 783 AGAGTNACAAAAGTGGAGCACAAGTCAAACCAGAAGGAACGGAGGAAGCCTGATGTCTGTT GGCACAGAGTAGCAGGTGAGCCGTGGTTTTTGGTGACATTGGGGGCAGAGTGGTGGTGGTGGAGGT TCTGCCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTCCAGGGGCTTGGCCTGT TCTGCCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTCCAGGGGCTTGG-CTGT GGCACAGAGTAGCAGGTGAGCCGTGGTTTTTGGTGACATTGGGGGCCAGAGTGGTGCAGGGT Human cDNA encoding a membrane or secretory protein clone PSEC0162. Human, secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; ss. ĸ Sugiyama T, GTGTTGCTGCATCTTCTTACGCAAAAAAAAAAAA 1291 Grerrecrecarcricriacecaaaaagacaaaa 1296 Kawai Y, Isogai T, Nishikawa T, standard; cDNA; 1320 99JP-00194179. 2000JP-00118775. 2000JP-00183766. 07-JUL-2000; 2000EP-00114090 23-MAY-2001 (first entry) (HELI-) HELIX RES INST. WPI; 2001-093989/11. P-PSDB; AAB88406. Ното варіепв EP1067182-A2 08-JUL-1999; 11-JAN-2000; 02-MAY-2000; 10-JAN-2001 1017 1142 1202 837 843 897 903 957 963 1023 1077 1083 1137 1197 1257 1262 AAF93833; AAF93833 Ota T, RESULT 셤 à g ò a ò 셤 ठ 셤 ઠે 셤 ò 셤 셤 à 셤 ઠે

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which encode human secretory or membrane proteins represented by AAB88317

AAR88419. Included in the invention are primers AAF93917 - AAF94295 and
AAF82232 - AAF87235 which are used to isolate the CDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and cDNA sequences, which can
be used in vaccines. The polymucleotide sequences can be used in gene
therapy. The polymucleotide sequences and the proteins they encode may be
therapy. The polymucleotide sequences and the proteins they encode may be
therapy. The polymucleotide sequences may also be used as DNA probes
the and in appropriate secretory protein/membrane protein expression. The
nucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerses chain reactions (PCR)) to detect
and quantitate the presence of similar nucleic acid sequences in samples.
They may also be used as antigens in the production of antibodies
complementary becaused their role in metabolism. The
polypeptides may be used as antigens in the production of antibodies
companies of expression and activity. The antibodies and antagonists
companies them and in assays to identify modulators (agonists and
activity. The antibodies may also be used as therapeutic agents to down regulate expression and
activity. The antibodies may also be used as diagnostic agents for
detecting the presence of the polypeptides in amples (e.g. by enzyme
companies). The antibodies may also be used as diagnostic agents for
detecting the presence of the polypeptides in amples (e.g. by enzyme
companies include rheumatoid arthritis and diabetes
                                                                          - AAF93916
Claim 1; SEQ ID NO 179; 609pp + Sequence Listing; English.
                                                                          invention relates to nucleic acid sequences AAF93744
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Sequence 1320 BP; 332 A; 359 C; 370 G; 259 T; 0 U; 0 Other;

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CTGGGGGAGGAGGCGAAGCGACGACGATGGCTCCGCGGGCACTCCCGGGGTCCGCCG 123
                                                                                                                                                                                              TCCTAGCCGCTGCTGTTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGGACA 183
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69.7%; Score 900; DB 5; Length 1320; larity 99.4%; Pred. No. 4.5e-251; Conservative 0; Mismatches 5; Indels (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to novel human secretory proteins or membrane proteins, and their coding sequences. The present sequence is one such coding sequences of the invention are useful for examination and diagnosis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins Note: The sequence data for this patent did not form part of the printed specification, but was obtained from sequence information supplied by the European Patent Office.
TGTGTCATCGGTGTAGGCACAAGCGGGGCACTTTATAAAGCCCACTAACAAGTCCAGAG
                                                                                                                   AGAGCAGACCACGGCGCCAAGGCGAGGTCCACGGTCCTTTCTGTTGGCAGATTTAGAGTTA
                                                                                                                                                     CAAAAGTGGAGCACAAGTCAAACCAGAAGGAACGGAGAAGCCTGATGTCTTTAGTGGGG
                                                                                                                                                                                 781 CAAAAGTGGAGCACAAGTCAAACCAGAAGGAACGGAGAAGCCTGATGTCTGTTAGTGGGG
                                          TGTGTCATCGGTGTAGGCACAAGCGGTGGCACTTTATAAAGCCCACTAACAAGTCCAGAG
                                                                                               724 AGAGCAGACCACGCCCAAGGCGAGGTCACGGTCCTTTCTGTTGGCAGATTTAGAGTTA
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11-JAN-2000; 2000JP-00118775.
02-MAY-2000; 2000JP-00118776.
07-JUL-2000; 2000BP-00114090.
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                                                           Length 1320;
                     Sequence 1320 BP; 332 A; 359 C; 370 G; 259 T; 0 U; 0 Other;
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                                                         Score 900; DB 14;
Pred. No. 4.5e-251;
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The invention relates to an isolated polynuclectide encoding a polypeptide with biological activity. The polynuclectides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and other traits, to assess biodiversity, as nutritional sources or supplements. The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides are useful for raising antibodies, as markers for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or cregeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents cDNA encoding a novel human protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polynucleotides and secreted proteins, useful for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and nerve tissue growth or regeneration, in wound healing, and in tissue repair and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGACGCGCGATGCCTCCCCGGGCACTCCCGGGGTCCCCCTCCTAGCCGCTGCTGTT 120
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                                                                                                                                                                                                                                                                                                                  myeloid cell disorder; lymphoid cell disorder;
bone cartilage tissue growth; tendon tissue growth;
ligament tissue growth; nerve tissue growth; regeneration; wound healing;
tissue repair; tissue replacement; burn; incision; ulcer; cancer; human;
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ou P, Drmanac RT,
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Pred. No. 1.8e-248;
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Ghosh M, Kue AJ, Wehrman T, Weng G, Zhou P,
Haley-Vicente D;
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100.0%;
   standard; cDNA; 1218
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The present invention provides the protein and coding sequences of novel proteins from a variety of organisms, including human, dog, cat, horse, cow, pig, hamster, monkey, macaque, yeast, bacteria, fruit fily, see urchin and tomato. These were derived from expressed sequence tags (ESTs from the organism of interest. They can be used in diagnostics, forensics, gene mapping, identification of mutations, to assess biodiversity and for nutritional purposes. The present sequence is a cDN of the invention
                                                                                                                                                                         Isolated polypeptide for treatment of diseases, diagnostics, raising antibodies and research use.
                                                                                                                                                                                                         Claim 1; Page 522; 1275pp; English.
                             25-JAN-2000; 2000US-00491404.
17-JUL-2000; 2000US-00617746.
03-AUG-2000; 2000US-00631451.
15-SEP-2000; 2000US-00663870.
                                                                                                          Zhou P, (
A, Zhang
                                                                                                         Liu C, Zh
Drmanac RA,
                                                                                                                                         WPI; 2001-476164/51
P-PSDB; AAM23972.
                                                                                     (HYSE-) HYSEQ INC
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                                                                                                                                                                       GCGATGGCTCCGCGGGGCACTCCCCGGGGTCCGCCGTCCTAGCCGCTGCTGTCTTCGTGGGA
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                                                                                         GCGATGGCTCCGCGGGCACTCCCGGGGTCCGCCGTCCTAGCCGCTGCTGTCTTCGTGGGA
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                                                             1;
                                Length 861;
Sequence 861 BP; 216 A; 214 C; 265 G; 166 T; 0 U; 0 Other;
                                                             Indele
                            Score 827.8; DB 4;
Pred. No. 3.9e-230;
0; Mismatches 12;
                            Query Match
Best Local Similarity 98.5%;
Matches 846; Conservative 0
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Human; sheep; plg; cow; fruit fly; yeast; hamster; macaque; horse; tomato; monkey; dog; sea urchin; expressed sequence tag; EST; diagnostics; forensic test; gene mapping; genetic disorder; biodiversity; gene therapy; nutrition; ss.

WO200154477-A2

Homo

02-AUG-2001

Human EST-derived coding sequence SEQ ID NO: 488.

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The polynucleotides may also be used as molecular weight markers, chromosome markers or map related gene positions, or as an antigen to raise anti-DNA antibodies or elicit immune response. The polypeptides useful for raising antibodies, as marker for tissues in which the corresponding polypeptide is expressed, for re-engineering damaged or diseased tissues, for treating myeloid or lymphoid cell disorders, in bone cartilage, tendon, ligament and/or nerve tissue growth or regeneration, in wound healing, in tissue repair and replacement, in healing of burns, incisions and ulcers, and in treating cancer. The present sequence represents a novel human expressed sequence tag, EST.
                                                                                                                                                                                                                                                   Sequence 861 BP; 216 A; 214 C; 265 G; 166 T; 0 U; 0 Other;
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                           601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          forensic; nutritional source; damaged tissue; diseased tissue; myeloid cell disorder; lymphoid cell disorder; bone cartilage tissue growth; tendon tissue growth; ligament tissue growth; nerve tissue growth; regeneration; wound healing; tissue repair; tissue replacement; burn; incision; ulcer; cancer; human; ss; gene; BST; expressed sequence tag.
                                                                                                                                                                                                                                                                                            GGTCACGGTCCTTTCTGTTGGCAGATTTAGAGTTACAAAAGTGGAGCACAAGTCAAACCA 781
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TCTGCATACGGTGGGGGGTGTTGTCGAGAGGATGTGTGTCATCGGTGTAGGCACAAGCG
                                                                                                                                                                                                     GTGGCACTTTATAAAGCCCACTAACAAGTCCAGAGAGAGCAGACCACGCGCCCAAGGCGA
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Drmanac RT,
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Weng G, Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human expressed sequence tag, EST #58.
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Wehrman T,
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Ghosh M, Xue AJ, V
Haley-Vicente D;
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P-PSDB; ADI21579.
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64.1%; Score 827.8; DB 10; Length 861; 98.5%; Pred. No. 3.9e-230; tive 0; Mismatches 12; Indels 1;
                         Best Local Similarity 98.5
Matches 846; Conservative
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other

The invention relates to an isolated polynucleotide encoding a polypeptide with biological activity. The polynucleotides and polypeptides are useful in diagnostics, forenaics, gene mapping, identification of mutations responsible for genetic disorders and othe traits, to assess biodiversity, as nutritional sources or supplements.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which encode human secretory or membrane proteins represented by AAB88317

AAB88419. Included in the invention are primers AAF93917 - AAF94295 and
AAF62235 - AAF62235 which are used to isolate the CDNA sequences of the
invention. The invention also includes methods for the production of
antibodies directed against the proteins, and CDNA sequences, which can
be used in vaccines. The polymucleotide sequences can be used in gene
therapy. The polymucleotide sequences and the proteins they encode may be
used in the prevention, treatment and diagnosis of diseases associated
with inappropriate secretory protein/membrane protein expression. The
nucleic acids and complementary sequences may also be used as DNA probes
in diagnostic assays (e.g. polymerses chain reactions (PCR)) to detect
and quantitate the presence of similar nucleic acid sequences in samples.
They may also be used to study the expression and function of secretory
proteins/membrane polypeptides and their role in metabolism. The
polypeptides may be used as antigens in the production of antibodies
contains and in assays to identify modulators (agonists and
antiagonists) of expression and activity. The antibodies and antagonists
may also be used as therapeutic agents to down regulate expression and
cativity. The antibodies may also be used as diagnostic agents for
detecting the presence of the polypeptides of diseases which may be
linked immunosorbant assay (ELISA). Examples of diseases which may be
treated include rheumatoid arthritis and diabetes
                                                                                                                                                                                                 Primer specific for DNA encoding secretory/membrane protein SEQ ID 466.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to nucleic acid sequences AAF93744 - AAF93916
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                                                                                                                                                                                                                              Human; secretory protein; membrane protein; vaccine; gene therapy; rheumatoid arthritis; diabetes; PCR primer; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; SEQ ID NO 466; 609pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sugiyama T,
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GGCAACACCTGTGAAGAGA 887
                           842 GCCAACAACTTGTGAGAGA 860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isogai T, Nishikawa T,
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02-MAY-2000; 2000JP-00183766.
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                                                                                                        AAF94032 standard; DNA; 726
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CTGGGGAAGGAGGAGAAGGAAGCGCGGGGATGGCTCCGCGGGGCACTCCCGGGGTCCGCCG
                                                                                                                 184 ATGGGAGCCGCACATTGCACTCCAGAACAGACGACCCCGTCGCCCAGCAACGATA
                                                                                                                                       ATGGGAGCCGCGCATTGCACTCCAGAACAGAGACGACCCCCGTCGCCCAGCAACGATA
                                                                                                                                                                                   CTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTCTTTATCATGG
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                                                                                                                                                                                                                                                      GICTCTTTGGCGTCCTCATTTGCCACCTGCTTAAGAAGAAAGGCTATCGTTGTACAACAG
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                                               124 TCCTAGCCGCTGCTGTCTTCGTGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGGACA
                                                                                                                                                                                                                                                                                                                          AAGCAGAGCAAGATATCGAAGAGAAAAGGTTGAAAAGATAGAATTGAATGACAGTGTGA
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Best Local Similarity 98.3 Matches 712; Conservative

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19-MAY-2003;
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08-JUL-2003;
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                                                                                                                                                                                                                              The present invention relates to novel human secretory proteins or membrane proteins, and their coding sequences. The coding sequences of the invention are useful for examination and disponsis of abnormality of the human secretary proteins and in gene therapy methods. The coding sequences and proteins are useful as candidates for medicines or as target molecules for developing medicines. Antibodies against the proteins of the invention are useful for treating diseases that are associated with the proteins. The present sequence is a 5'-end sequence of one such coding sequence of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was patent and acquence information supplied by the Buropean Patent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGGGAAGGAGGCGAAGCGAGGGGATGGCTCCGCGGGCACTCCCGGGGTCCGCCG
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                                                                                                                                        Novel isolated polynucleotide encoding human secretary proteins or membrane proteins, useful for examination and diagnosis of abnormality
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53.1%; Score 685.2; DB 14; Length 726; llarity 98.3%; Pred. No. 1.2e-188; Conservative 0; Mismatches 10; Indels 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 726 BP; 174 A; 192 C; 219 G; 138 T; 0 U; 3 Other;
                                                                             Sugiyama T,
                                                                             Kawai Y,
                                                                                                                                                                                                      Example 1; SEQ ID NO 466; 1240pp; English.
                                                                            T, Isogai T, Nishikawa T,
                                             (REAS-) RES ASSOC BIOTECHNOLOGY.
02-MAY-2000; 2000JP-00183766.
07-JUL-2000; 2000EP-00114090.
                                                                                                                                                                       human secretary proteins
                                                                                                         WPI; 2005-203865/22
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es 712; Conserv
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                                                                                     GTGTGTCATCCGGTGTAAGCACAANCGGTGGCCATTTATAAAGCCCCACTAACANGTCCAG
               CCAGGGAAGCACGTCTGTGGCCATCATCTGCATACGGTGGTGTTGTCAAAAGGGAT
CCAGGGAAGCACGTCTGTGGCCATCATCTGCATACGGTGGGCCGTGTTGTCGAGAGGGAT
                                                               GTGTGTCAT-CGGTGTAGGCACACAGCGGTGGCACTTTATAAAGCCCCACTAACAAGTCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               given in the specification, useful in preparing a composition for diagnosing or treating e.g., cancer, psoriasis or ulcerative colitis.
                                                                                                                                                                                                                                                                                                                                                                                         cytostatic; antipsoriatic; antiinflammatory; gene therapy; Nanodisc; proliferative disorder; inflammatory disorder; immune disorder; metabolic disorder; bone disorder; CNS disorder; cancer; psoriasis; ulloerative colitis; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New first nucleic acid molecule comprising a polynucleotide sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 486; 291pp; English.
                                                                                                                                                                                                                                                                                                                                                           Novel human polynucleotide segid 486.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FIVE-) FIVE PRIME THERAPEUTICS INC.
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2003US-0471306P.
2003US-0471336P.
2003US-048523P.
2003US-0485234P.
2003US-0486446P.
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2003US-0463732P.
2003US-0467199P.
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2003US-0493577P.
2003US-0505059P.
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comprising the polypeptide and acution comprising a carrier or abuffer and one or more compositions comprising the bulleter and one or more compositions comprising the polypeptide and a carrier or buffer; a cell comprising the polypeptide and a carrier or buffer; a cell culture medium comprising the polypeptide or transfected cells cransfected with the polypeptide or transfected or infected host cell; synthesisting a bandlands acrie of simultaneously-synthesised Nanodiscs and for synthesising a dynamic system; preparing a hydrophobic protein for determination of crystal structure; immunising a non-human animal; creening for modulators of pydrophobic protein activity, a diagnostic complement; determining the presence of the mucleic acid molecule or its biologically active fragment; an antibody to the polypeptide in a sample; an antibody specifically recognising, binding to or modulating the presence of the mucleic acid molecule or its biologically active fragment; an antibody and a carrier; a bacteriophage, a composition comprising the antibody and a carrier; a bacteriophage; and the bacteriophage; a non-human animal injected with the antibody; diagnosing a disease, disorder; syndrome, or condition comprising cancer, or proliferative, inflammency, immune, metabolic, contitions in a patient; a modulator composition comprising a modulator composition and a carrier; gene therapy; prophylactic or therapeutic treatment of a conditions in a patient; a modulator composition comprising a modulator composition and a carrier; gene therapy; prophylactic or therapeutic treatment of a cid molecule comprises a first polymeted sequence that encodes a first polymeted or the propypetide or the corrier; gene therapy; prophylactic corrier; a loolecule, where the fir
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Sequence 348 BP; 34 A; 121 C; 146 G; 47 T; 0 U; 0 Other;

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DB 13; Length 348;
                                    4; Indels
Score 172.6; DB 1;
Pred. No. 1.8e-39;
                                    0; Mismatches
 13.4%;
                                   Matches 175; Conservative
                    Local Similarity
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Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                 Oligonucleotide for detecting cytosine methylation SEQ ID NO 5597.
              ABQ19006 standard; DNA; 694 BP
                                                                      (first entry)
                                                                     12-JUL-2002
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WO200218632-A2 Homo sapiens.

methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonacieotides and/or peptide-nucleic acid (PNA) oligonace and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligonaces, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13110-1605. ABQ54121 represent genomic DNA sequences used to illustrate the method in the contral contral and contral contral contral contral control contro Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons 246 CGTCGGTTTCGGAGCGGTTTTGTTTTTCGAGCGCGGGGACGCGGCGTTTTGGGGGAGGAG 306 GGCGAAGCGACGCGCGATGGTTTCGCGGGTATTTTCGGGGGTTCGTCGTTTTAGTCGTTG Gaps invention describes a novel method for determining the degree ö 8.9%; Score 115.4; DB 6; Length 694; 11.2%; Pred. No. 1.2e-22; ve 0; Mismatches 31; Indels 0; 180 Sequence 694 BP; 74 A; 86 C; 302 G; 232 T; 0 U; 0 Other; CTGTCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG Claim 12; 56pp + Sequence Listing; 56pp; German. Guetig D; Berlin K, 01-SEP-2001; 2001WO-EP010074 01-SEP-2000; 2000DE-01043826. diagnosis and prognosis, comprosis complexes chemically treated DNA. disclosure of the invention Best Local Similarity 81.2%; Matches 134; Conservative Olek A, Piepenbrock C, (EPIG-) EPIGENOMICS AG WPI; 2002-371829/40. 07-MAR-2002. 136 Query Match 셤 ઠે 용 ò ઠે

305 365 76 GGCGAAGCGACGCGGCGATGGCTCCGCGGGCACTCCCGGGGTCCGCCGTCCTAGCCGCTG 135 75 Human, cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; Oligonucleotide for detecting cytosine methylation SEQ ID NO 5598. rretrircereceaecerecicaeirearecreerecrirecree 410 366 RESULT 15 셤

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DAN. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of cligomers, the degree of methylation is calculated. The method is used:

(1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastroineestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation. The method allows the methylation status of many C residues to be determined simultaneously. Abglistion attatus of many C residues to be determined simultaneously. Abglistion determining the degree of cytosine methylation described in the
                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; 56pp + Sequence Listing; 56pp; German.
                                                                                                                                                                                                                                                                                                                                      Guetig D;
                                                                                                                                                                                                                                                                                                                                      Berlin K,
SNP; cell differentiation; ds
                                                                                                                                                                                                                     01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                            01-SEP-2001; 2001WO-EP010074
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                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                          (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-371829/40.
                                                                                       WO200218632-A2
                                             Homo sapiens.
                                                                                                                                  07-MAR-2002.
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GCCGAAGCGACGCGGCGATGGCTCCGCGGGCACTCCCGGGGTCCGCCGTCCTAGCCGCTG 135 389 GGCGAAGCGACGCGGCGATGGTTTCGCGGGTATTTTCGGGGTTCGTTTTAGTCGTTG 136 CTGTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGG 180 329 TIGITITICGTGGGAGGCGTCGTGAGTICGTCGTTGGTGGTTTCGG 285 92 셤 g ઠે ò

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Gaps 0; cecceecteceasececterecenteceasececeasececececereases 75

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Query Match 8.9%; Score 115.4; DB 6; Length 694; Best Local Similarity 81.2%; Pred. No. 1.2e-22; Matches 134; Conservative 0; Mismatches 31; Indels 0;

Search completed: February 23, 2006, 14:48:06 Job time : 791 secs

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                                                                                                                                                                                                                                                                                                         Description
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GenCore version 5.1.7
(c) 1993 - 2006 Biocceleration Ltd.
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Listing first 45 summaries
                                                                                                nucleic search, using sw model
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/tissue_type="ADDLT BRAIN"
/dev_stage="adult"
/clone_lib="Homo satist"
/note="Organ: brain; Vector: pCMVSPORT 6; lst strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."

ORIGIN

1. .898 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="CS0DN002YB14"

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ACCESSION VERSION KEYWORDS	BX4	BX463460 BX463460 EST.			070	031			
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REFERENCE	ч	(раве	38 1	(bases 1 to 898)	8				
AUTHORS	17,1	e.	당.	ber, c		Li,w.B., Gruber, C., Jessee, J. and	and Polayes, D.		
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Ното варіепв

Hominidae, Homo.

1 (bases 1 to 882)

14 HAGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection Unpublished (1999)

REFERENCE

Contact: Rober Strausberg, Ph.D.

Email: cgapbs-remail nih,gov
Tissue Procurement: DcrD/DTP
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM780 row: j column: 12
High quality sequence stop: 825.

/organism="Homo sapiens"

1. .882

Bource

FEATURES

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KEYWORDS
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            Length 898;
                                    9; Indels
         ; Score 855.2; DB 5;
; Pred. No. 8.8e-221;
15; Mismatches 9;
           66.2%;
97.1%;
                                    Conservative
                        Similarity
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Matches 873;
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882 bp mRNA linear EST 20-SEP-2000 G01582045F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3936491 5', BE792154

DEFINITION ACCESSION VERSION

RESULT 2 BE792154 LOCUS

BE792154.1 GI:10213352

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                                                                    GTGACACTGTTGGGCAAATCGTCCACTACATCATGAAAAATGAAGCGAATGCTGATGTCT
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Score 756.8; DB 5;
Pred. No. 4.8e-194;
9; Mismatches 13;
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58.6%;
llarity 96.7%;
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 Query Match
Best Local Simil
Matches 803; C
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
Z rue Gaston Cremieux, P. 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BX423892 Homo sapiens ADULT BRAIN Homo sapiens cDNA clone CSODN002YB14 5-PRIME, mRNA sequence.
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/dev stage="adult"
/clone_lib="Homo sapiens ADULT BRAIN"
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-estrand cDNA was digested with Not I and cloned into the Not I and ECONY sites of the pCMVSPORT 6 vector. Library was not normalized."
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Mammalia, Butheria, Buarchontoglires, Primates, Catarrhini,
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GCAAATCGTCCACTACATCAAAAATGAAGCGAATGCTGATGTCTTAAAGGCGATGGT
                                                                                                   GCCAGTGAGTCCTGGGCCTTTGTCACCAGGGGGGGGCCCAGGGAAGCACGTCTGTGGCCA
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                                  AGCAGATAACAGCCTGTATGATCCTGAAAGCCCCGTGACCCCCAGCACACCAGGGAGCCC
                                                      This sequence belongs to sequence cluster 2573.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS1AN001ZD08QP1&c=2573.r.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hominidae, Homo.

1 (bases 1 to 882)

1.4. H.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 13, 2003 this sequence version replaced gi:30655585.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DN002YB14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              division of Invitrogen.
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BX423892
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599 672 732

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778

842

DMYLYS48 10-MAR-2002 AGENCOURT 6761913 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5748847 5', mRNA Sequence. Homo saplens Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

ORIGIN

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10. :620

| Corganism="Macaca mulatta" |
| Mol_type="MRNA" |
| Mol_type="MRNA" |
| Ab Aref="taxon:5944" |
| Albone="IMAGE:5331301" |
| Alsoue_type="Mypothalamus" |
| Alab host="DH10B" (phage-resistant)" |
| Albone="Norgan:brain, Vector: pCMV-SPORT6.1; Site_1: Not1; |
| Mole="Organ:brain, Vector: pCMV-SPORT6.1; Site_1: Not1; |
| Anerage insert size 2.2 kb. Constructed by Invitrogen. |
| Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbe-remail.nih.gov
cDNA Library Preparation:
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NOI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
Info@lnage.llnl.gov
Plate: LLAM11840 row: O column: 14
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NISC kkloh07.yl NCI CGAP Brn72 Macaca mulatta cDNA clone
IMAGE:5331301 5', mRNA sequence.
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
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1 (bases 1 to 620)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
542 CCAGCACACCAGGGAGCCCGCCAGTGAGTCCTGGGCCTTTTGTCACCAGGGGGAGCCCCAG
                                                                                                                                                                                                                           GGAAGCACGTCTGTGGCCATCATCT-GCATACGGTGGCGCGGTTGTCGAGAGGGATGTG
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46.0%; Score 594.4; DB 5;
Best Local Similarity 97.4%; Pred. No. 5.9e-150;
Matches 604; Conservative 0; Mismatches 16;
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Seg primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Macaca mulatta
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 726.8; DB 3; Length 1000;
Pred. No. 7e-186;
0; Mismatches 24; Indels 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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Best Local Similarity 95.9%;
Matches 800; Conservative (
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/ sexe "male"
/ tissue_type="dorsal root ganglia"
/ tissue_type="dorsal root ganglia"
/ dev_stage="dorsal root ganglion"
/ lab_host="bulos"
/ lab_host="bulos"
/ clone_lib="Lupski_dorsal root ganglion"
/ clone_lib="Lupski_dorsal root ganglion"
/ note="vector: pCWV-SpORTG (Life Technologies); Site_l:
Not1; Site_2: Sall; CDNA made by oligo-dT priming.
DirectionaTly cloned using the following adaptors:
5. TCGACCACGCGTCCG-3. and
5. GACTAGTTCTAGATCGCAGGGGCGCCCT(IS)-3. Size selected >
1 kb for average insert length 1.7 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6178627"
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AGENCOURT 8121018 Lupski dorsal_root_ganglion Homo sapiens cDNA clone IMAGE:6178627 5', mRNA sequence.
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298 418 538 598 718 238 241 358 361 421 478 658 661 777 301 481 541 601 721 CATGGGTCTCTTTGGCGTCCTCATTTGCCACCTGCTTAAGAAGAAGAAGAAGGCTATCGTTGTAC CGATACTGGGGAATGGACACCCAGAATATTGCATACGCGCTTGTCTTTTAT **AACAGAAGCAGAGCAAGATATCGAAGAGGAAAAGGTTGAAAAGATAGAATTGAATGACAG** TGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCATGAAAATGAAGC GAATGCTGATGTCTTAAAGGCGATGGTAGCAGATAACAGCCTGTATGATCCTGAAAGCCC CGTGACCCCCAGCACACCAGGGAGCCCGCCAGTGAGTCCTGGGCCTTTGTCACCAGGGGG CGTGACCCCCAGCACACCAGGGAGCCCGCCAGTGAGTCCTCTGTGCCTTTGTCACCAGGGGG GACGCCAGGGAAGCACGTCTGTGGCCATCATCTGCATACGGTGGTGGTTGTCGAGAG GACGCCAGGGAAGCACGTCTGTGCCATCATCTGCATACGGTGGGCGGTGTTGTCGAGAG GGATGTGTGTCATCGGTGTAGGCACAAGCGGTGGCACTTTATAAAGCCCACTAACAAGTC GGATGTGTGTCATCGGTGTAGGCACAAGGGGTGGCACTTTATAAAGCCCACTAACAAGTC GGACAATGGGAGCCGCACATTGCACTCCAGAACAGAGACGACCCCCGTCGCCCAGCAA CGATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTCTTTAT CATGGGTCTCTTTGGCGTCCTCATTTGCCACCTGCTTAAGAAGAAAAGGCTATCGTTGTAC CAGAGAGAGCAGACCACGCCCCAAGGCCGAGGTCA-CGGTCCTTTCTGTTGGCAGATTTA Gaps ä Length 874; 6; Indels Query Match
Best Local Similarity 98.9%; Pred. No. 6.4e-150;
Matches 609; Conservative 0; Mismatches 6;

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DN948289 815 bp mRNA linear EST 29-APR-2005
AGENCOURT_50111126 NCI_CGAP Pr49 Rattus norvegicus cDNA clone
IMAGE:7932431 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5-, and 7-days
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                                                                                                                                                                         366 AATGACAGTGTGAGAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCAAAA 425
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                                                                                                                                                                                                                                           411 AATGACAGTGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCAAAA 470
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Sulfoguatini, multidae; murinae; katub.

National Institute of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics

National Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 RmloAO7 BethedGa, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeff Green/Paturu Kondaiah, NCI.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM16355 row: k column: 21

High quality sequence stop: 792.
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post-castration"
/dev_stage="adult, 11 week"
/lab host="H10B (T1 phage-resistant)"
/lab host="NGI_CGAP_Pr49"
/note="Organ: prostate; Vector: pCMV-SPORT6.1; Site_1:
Not1; Site_2: ECCRV; Cloned unidirectionally. Primer:
Oligo dT. Pool of 3 primary libraries: NGI_CGAP_Pr30
(ventral prostate from 11 wk male, 3 days
                                                                              246 TICITIATCATGGGTCTCTTTGGCGTCCTCATTTGCCACCTGCTTAAGAAGAAGAAGAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GAAAGCCCCGTGACCCCCAGCACCACCAGGGAGCCCGCCAGTGAGTCCTGGGCCTTTTGTCA
                                                                                                                                                                                                                                                                                                                                         471 AATGAAGCGAATGCTGATGTCTTAAAGGCGATGGTAGCAGATAACAGCCTGTATGATCCT
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Bute
Mammalia, Euheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Rattus.
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/organism="Rattus norvegicus"
/orjanism="Rattus norvegicus"
/ol_Xref="taxon:10116"
/clone="IMAGE:7932431"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              591 CCAGGGGGACGCCAGGGAAGCACGTCTGTGG 622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGGGGGACGCCAGGGAAGCACGTCTGTGG 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus norvegicus (Norway rat)
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DKUU45/3
TC104761 Human placenta, large insert, pCMV expression library Homo appiens cDNA clone TC104761 5' similar to Homo sapiens hypothetical protein LOC253981 (LOC253981), mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="vector: pcWv6-XL4; Site 1: EcoR1; Site_2: Xhol/Sal1 compatible end ligatio; Oligo-dT primed reverse transcription optimized for large and GC rich mRNA transcripts, cDNA size selection, optimized ligation for large inserts into mammalian expression vector, random clones selected for end sequence verification of full-length genes"
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1 (bases 1 to 577)

1 bases 1 to 577)

2 bixett, C., Cho, J., Gau, Y., Hamer, R., Kelly, S., Kovacs, K., Liu, L., Liu, X., Porter, J., Sachs, A., Shu, Y., Sun, Z., Wong, J., Wu, M., Zhang, X., Jay, G. and He, W.

2 kang, X., Jay, G. and He, W.

2 cDNA libraries optimized for large and rare transcripts

Unpublished (2005)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Placenta"
/clone_lib="Human placenta, large insert, pCMV expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACGCGCCCTGGGGGAGGAGGCGAAGCGACGCGGCGATGGCTCCGCGGGCACTC 110
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High Throughput cDNA Cloning
OriGene Technologies, Inc. (www.origene.com )
6 Taft Court, Suite 100, Rockville, MD 20850, USA
Tel: 301 340 3188
Fax: 301 340 8606
Email: cDNA@origene.com
This EST submission is part of an on-going human full-length
cloning project at OriGene Technologies, Inc.
Please contact OriGene for access.
OriGene Technologies, Inc.
Set prime: MA 40-3188
http://www.origene.com
Set prime: pCWV6 Sprime forward vector primer, OriGene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CCCAGCAACGATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTG
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Pred. No. 2.5e-143;
0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="TC104761"
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Matches 570; Conservative
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post-castration, average insert size 2 kb), NCI_CGAP_Pr40 (ventral prostate from 11 wk male, 5 days post-castration, average insert size 1.6 kb) and NCI_CGAP_Pr41 (ventral prostate from 11 wk male, 7 days post-castration, average insert size 2.5 kb). Constructed by Life Technologies/Invitrogen. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                  TCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGGACAATGGGAGCAGCCGCA 198
                                                                                                                                                                                                                                                                                             180
                                                                                                                                                                                                                                                                                                                     CATTGCACTCCAGAACAGACGACCCCGTC---GCCCAGCAACGATACTGGGAATGGAC 255
                                                                                                                                                                                                                                                                                                                                      ACCCAGAATATATGCATACGCGCTTGTCCCCGTGTTTATCATGGGGTCTCTTTGGCG 315
                                                                                                                                                                                                                                                                                                                                                                                              TCCTCATTTGCCACCTGCTTAAGAAGAAAGGCTATCGTTGTACAACAGAAGCAGAGGAAG 375
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                                                                                                               Score 554.2; DB 8; Length 815;
Pred. No. 5.3e-139;
0; Mismatches 153; Indels 3
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                                                                                                              42.9%;
                                                                                                                            Similarity 80.9
                                                                                                                                      629;
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EST 30-DEC-2003

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RESULT 9 BP438847 LOCUS

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/organism="Sus scrofa"
/mol_type="mRNA"
/mol_type="mRNA"
/clone="lawGol079F11"
/tissue_type="lung"
/clone_tiage="adult"
/clone_lib="full-length enriched swine cDNA library, adult lung"
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Low quality bases were trimmed based on the quality values.
                                                                                                                                                                                                  1 (bases 1 to 684)
Ueniabil,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
Ueniabil,H., Eguchi,T., Suzuki,K., Sawazaki,T., Toki,D., Shinkai,H.,
PKDE (Pig EST Data Explorer): construction of a database for ESTs
derived from porcine full-length cDNA libraries
Nucleic Acids Res. 32 (1), D484-D488 (2004)
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Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
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                    Sue
                                                                                                                                                                                                                                                                                                                                Animal Genome Laboratory, Genome Research Department
National Institute of Agrobiological Sciences
2 Ikenodai, Taukuba, Ibaraki 305-8602, Japan
Tel: +81-29-818-8627
Eax: +81-29-818-8627
Email: huenishidaeffer.go.jp
EST project with full-length enriched cDNA libraries carried out
Animal Genome Research Program (Japan) by National Institute of
Agrobiological Sciences and STAPF-Institute
Single pass sequencing of clones derived from oligo-capped cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCTGTCCCTGTGTTTTTTATCATGGGTCTCTTTGGCGTCCTCATTTGCCACCTGCTTAA
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BP438847 full-length enriched swine cDNA library, adult lung scrofa cDNA clone LNG010079F11 5', mRNA sequence.
BP438847
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0; Mismatches 89;
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Canis familiaris
Bukaryota: Metazos; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                                                                                                                                                        TACGCGCTTGTCCCTGTGTTCTTTATCATGGGTCTCTTTTGGCGTCCTCATTTGCCACCTG 332
                                                                                                                                                                                                                                                       CTTAAGAAGAAAGGCTATCGTTGTACAACAGAAGCAGAGCAAGATATCGAAGAGGAAAAG 392
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                                                         GTGAGTTCGCCGCTGGTGGCCGCCGACAACACTGGTAGCCACACGTTACACTCCCGAGCA
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                                GTGAGTTCGCCGCTGGTGGCTCCGGACAATGGGAGCAGCCGCACATTGCACTCCCAGAACA
                                                                                                                             GAGACGACCC---CGTCGCCCAGCAACGATACTGGGAATGGACACCCAGAATATATTGCA
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LIB38534_030_A09_T7_1 LIB38534 Canis familiaris cDNA clone
LIB38534_30_A09, mRNA sequence.
DN382824
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Direct Submission (Staten, N.R.)
Unpublished (2005)
Contact: Nick Staten
Tel: 636 247 685
Email: nicholas.F. staten@pfizer.com.
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/db xref="taxon:10090"
/clone="IMAGE:5354671"
/sex="female, virgin"
/tissue_rype="infiltrating ductal carcinoma"
/tissue_rype="infiltrating ductal carcinoma"
/tispue:rype="infiltrating ductal carcinoma"
/tispue:rype="infiltrating ductal carcinoma"
/tispue:rype="infiltrating ductal
/tispue:rype="infiltrating"
/tispue:rype
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603314531F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:5354671 5',
BI691144
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S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11901 row: m column: 08
High quality sequence stop: 753.
517
                                                                                                      CCTGTATGATCCTGAAAGCCCTGTGACCCCCAGCACTCCTGGGAGCCCGCCGTGGGCCC 544
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Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus.
                                                                        CTACATCATGAAAAATGAAGCGAATGCTGATGTCTTAAAGGCGATGGTAGCAGATAACAG
                                                                                                                                                                     CCTGTATGATCCTGAAAGCCCCGTGACCCCCAGCACACAGGGAGCCCGCCAGTGAGTCC
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Pred. No. 3.6e-121;
0; Mismatches 119;

    .906
    /organism="Mus musculus"

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/strain="FVB/N"
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Best Local Similarity 82.4%;
Matches 573; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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ATCTGCATACGGTGGGCGGTGTTGTCGAGGATGTGTGTCATCGGTGTAGGC-ACAAG 686
                                                                                                                                                                                                                                                                                                                                              Score 460.2; DB 3;
Pred. No. 1.8e-113;
0; Mismatches 153;
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 79.4%;
Matches 620; Conservative 0
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                                                                                                                                             CCTGGGGGAGGAGGCGACGCGGCGATGGCTCCGCGGGCACTCCCGGGGTCCGCC 122
                                                                                                                                                                                        GTCCTAGCCGCTGCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGGAC 182
                                                                                                                                                                                                                                 AATGGGAGCAGCCGCACATTGCACTCCAGAACAGAGACGCCCCGTCGCCCAGCAACGAT 242
                                                                                                                                                                                                                                                                             GGTCTCTTTGGCGTCCTCATTTGCCACCTGCTTAAGAAGAAAGGCTATCGTTGTACAACA 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                          542
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                                                                                                                                                                                                                                                                                                                                                                                                              AATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATGAAAAATGAAGCGAAT 482
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1 (bases 1 to 795)
NIH-MGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCTGATGTCTTAAAGGCGATGGTAGCAGATAACAGCCTGTATGATCCTGAAAGCCCCGTG
                                                                                                                         Gapa
/mol_type="mRNA"

/db_xref="texon:9615"
/clone="tiB39634 30 A09"
/tissue_type="unknown"
/lab_host="DH108"
/clone lih="till="lab"
/note="Vector: pSPORT1; Site_1: Sal1; Site_2: Not!"
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                                                                                                 Length 626;
                                                                                                                        Indele
                                                                                                37.1%; Score 479.6; DB 8;
86.2%; Pred. No. 9.3e-119;
ive 0; Mismatches 85;
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Mus musculus
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                                                                                                           al Similarity 86.2
530; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BI689796
                                                                                                 Query Match
Best Local S:
Matches 530
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/note="Organ: mammary; Vector: pCWV-SPORT6; Site 1: Sall;
/note="Organ: mammary; Vector: pCWV-SPORT6; Site 2: Not!; Cloned undirectionally. Primer: Oligo dT.
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH
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  (MGC)
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                                                                        Email: cgapbe-remail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can l
found through the I.M.A.G.B. Consortium/LIANL at:
http://image.llnl.gov
Plate: LiAMN1905 row. c column: 03
High quality sequence stop: 717.
National Institutes of Health, Mammalian Gene Collection
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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| Ocganism="Mus musculus"
| Ocganism="Mus musculus"
| Otrain="FVB/N"
| Ob xref="taxon:10000"
| Clone='IMAGE:5355962"
| Gex="female, virgin"
| Lissue type="infiltrating ductal carcinome"
| Clope taye="5 months"
| Clope taye="5 months"
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81.0%; Pred. No. 5.9e-112;
ive 0; Mismatches 124;
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Best Local Similarity 81.03
Matches 542; Conservative
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Butharia, Maracas, Chordata, Craniata, Vertebrata; Euteleostomi,
Mammalia; Eutheria; Euarchontoglires, Glires; Rodentia;
Sciurognathi; Muroidas; Muridae; Murinae; Mus.
1 (bases 1 to 680)
Scientali, Muroidas; Muridae; Murinae; Mus.
2 (bases 1 to 680)
Schodach, Y. Garton, N., Saito, R., Suzuki, H., Yamanaka, I.,
Kiyosawa, H., Yagi, K., Tomatu, Y., Hasegawa, Y., Nogami, A.,
Schombach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bult, C.,
Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,
Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusic, V.,
Chotha, C., Corbani, E., Cousins, S., Dalla, E., Dragani, T.A.,
Pletcher, C.F., Forrest, A., Frazer, K.S., Gasterland, T.,
Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,
Kawaii, H., Kawasawa Y., Kedzierski, R.M., King, B.L., Konagaya, A.,
Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,
Maltais, L., Marchiouni, L., McKenzie, L., Mixi, H., Nagashima, T.,
Numata, K., Okido, T., Pavan, W. J., Pertea, G., Pesole, G.,
Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,
Sandelin, A., Schneider, C., Semple, C.A., Setcu, M., Shimada, K.,
Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.
Verardo, R., Wagner, L., Wahlesteet, C., Wang, Y., Wangisawa, M.,
Sakazume, N., Sato, K., Shiraki, T., Wani, K., Kawai, J., Alzawa, K.,
Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,
Rogers, J., Birney, E. and Haysshizaki, Y., Wanagisawa, M., Satoxi, Condo, T.
Rogers, J., Birney, E. and Haysshizaki, Y., Waterston, R., Lander, E.S.,
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNs
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BX754410 RIKEN full-length enriched, osteoclast-like cell Musmusculus cDNA clone 1420039H17 5', mRNA sequence.
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The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216
Fax: 81-45-503-9216
                                                 GAGGICACGGICCITICIGITGGCAGATITAGAGTTACAAAAGIGGAGCACAAGICAAAC 806
  ATCTGCACACAGTGGGAGGTGGCGTTGAACGGGATGTGTGCCAGCGATGCAGGCAACAAG 615
                                                                                             CGATGGCACTTCATAAAACCCACCATCAAGACCACAGAG-GGACGGCACACGCGACAAGGC 674
                                                                                                                                                                                        GAGGTCACCGTCCTCTGTGGGCAGGTTCACAGTCACGAAAGTGGAGCCACAAGTCAAAT 734
                                                                                                                                                                                                                                                                                      CAGAAGGAGCGCAGAACTTTGATGTTCTGTCAGTGGCCATTGAAGTGTCACCGGGGATGT 794
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Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Carninci,P.,
                                                                                                                                                                                                                                          CAGAAGGAACGGAGAAGCCTGATG-TCTGTTAGTGGGGCTGAAACCGTCAATGGGGAGGT
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Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKBN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library was prepared and sequenced in Mouse Genome CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. 310 Fukuda,S., Hashizume,W., Hayashida,K., Hirozane,T., Hori,F., Imotani,K., Ishi,Y., Itoh,M., Kagawa,I., Kawai,J., Kojima,Y., Kodo,S., Komo,H., Koya,S., Miyazaki,A., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Ohasto,N., Saito,R., Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K., Shiraki,T., Tagami,M., Takeda,Y., Waki,K., Watahiki,A., Muramatau,M. and Hayashizaki,Y. prepare mouse tissues. Tissues were provided by Takashi Ishikawa (Department of Surgery 131 CCGCACATTGCACTCCAGAACAGAGACGACCC---CGTCGCCCAGCAACGATACTGGGAA 250 TGGCGTCCTCATTTGCCACCTGCTTAAGAAAAAGGCTATCGTTGTACAACAGAAGCAGA 370 74 AGGGCGAAGCGACGCGGCGATGGCTCCGCGGCCACTCCCGGGGTCCGCCGTCCTAGCCGC 133 TGCTGTCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGGCTCCGGACAATGGGAAGAG 193 TGGACACCCGGAATACATCGCGTACGTGCTCGTCCCTGTGTTCTTCGTCATGGGTCTCCT 311 73 71 /mol_type="mRNA" /strain="CS7BL/6J" /db_xref="taxon:10090" /clone="1420039H17" /cell_type="osteoclast-like cell" /clone_lib="RIKEN full-length enriched, osteoclast-like 2 Yokohama City University 3-9 Fukuura, Kanazawa-ku, Yokohama 236-0004 Japan) whose assistance we gratefully acknowledge. Please visit our web site (http://genome.gsc.riken.go.jp) for further details. ccciscascicicas de la contra del la contra de la contra del la c AGGGCAGAGGGACGCGGCGATGGCTCTGTGGGGACTCCCGGGGTCCGCTGTGTGTTGCTGC TGGACACCCAGAATATATGCATACGCGCTTGTCCTGTGTTCTTTATCATGGGTCTCTT Gaps 3; Length 680; Indels

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/mol_type="mRNA"
/strain="NMR1"
/db xref="taxon:10090"
/clone="IMAGE:5330037"
/tissue_type="tumor, gross tissue"
/dev_stage="tumor, gross ti
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603285885F1 NCI_CGAP_Mam4 Mus musculus cDNA clone IMAGE:5330037 5',
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Bukaryota, Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Buarchontoglines; Glines; Rodentia;

Sciurognathi; Muroidea; Muridae; Murinae; Mus.

1 (bases 1 to 757)

1 Mag.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11837 row; j column: 22
High quality sequence stop: 741.
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BY754598 672 bp mRNA linear EST 17-DEC-2002
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Sciurognathi, Muzoidea, Muridae, Musinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suchiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: genome-resegge.riken.jp, URL:http://genome.gec.riken.jp/
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Direct Submission

Computational Analysis of Full-Length Mouse cDNAs Compared with
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Tissues were provided by Takashi Ishikawa ( Department of Surgery
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/clone_lib="RIKEN full-length enriched, osteoclast-like
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236-0004 Japan ) whose assistance we gratefully acknowledge.
Please visit our web site (http://genome.gsc.riken.go.jp) f
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Sequence 56, Application US/09205258
Patent No. 6525174
GENERAL INFORMATION:
TILLE OF INVENTION: 207 Human Secreted Proteins
FILE REFERENCE: PZ007P1
CURRENT APPLICATION NUMBER: US/09/205,258
CURRENT PILING DATE: 1998-12-04
EARLIER APPLICATION NUMBER: PCT/US98/11422
EARLIER PILING DATE: 1998-06-06
EARLIER PILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER APPLICATION NUMBER: 60/048,896
EARLIER PILING DATE: 1997-06-06
EARLIER PILING DATE: 1997-06-06 048,899 APPLICATION NUMBER: 60/048,900 FILING DATE: 1997-06-06 APPLICATION NUMBER: 60/048,901 EARLIER APPLICATION NUMBER: 60/048,901 EARLIER FILING DATE: 1997-06-06 EARLIER APPLICATION NUMBER: 60/048,892 048,882 /048,893 R FILING DATE: 1997-06-06
A APPLICATION NUMBER: 60/04
R FILING DATE: 1997-06-06
A PPLICATION NUMBER: 60/04
R FILING DATE: 1997-06-06
A APPLICATION NUMBER: 60/04 FILING DATE: 1997-06-06 -09-205-258-56 EARLIER P EARLIER P EARLIER P EARLIER P EARLIER P

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15639, 15993,

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1016 1136 1141 120 180 240 416 926 123 243 357 476 536 543 596 959 662 716 176 936 842 968 902 962 183 ATACTGGGAATGGACACCCAGAATATATTGCATACGCGCTTGTCCCTGTGTTTTTATCA 300 303 363 423 483 602 722 782 64 CGTCCTAGCCGCTGCTGTCTTCGTGGGAGGCGCCGTGAGTTCGCCGCTGGTGAGTTCGCCG GCCCTGGGGGAGGAGGGGGAA-CGACGGGGGCATGCCCCCGGGGGCACTCCCGGGGGTCCG ACAATGGGAGCAGCACACATTGCACTCCAGAACAGAGACGACCCCGGTCGCCCAGCAACG TGGGTCTCTTTGGCGTCCTCATTTGCCACCTGC---TTAAGAAGAAAGGCTATCGTTGTA CAACAGAAGCAGGAGGAAGATATCGAAGAAAAAAGGTTGAAAAGWTAGRATTGAATGAC AGTGTGAATGAAAACAGTGACACTGTTGGGCAAATCGTCCACTACATCATGAAAATGAA GGGACGCCAGGGAAGCACGTCTGTGGCCATCATCTGCATACGGTGGGGCGGTGTWGTCGAG GGAAGTGGGAGAGCTTTCCTTGACCCAGGAAGACTGAGGGGGACTGAACATGATTACTTG 191 ACAATGGGAGCACCCGCACATTGCACTCCAGAACAGAGACGACCCGTCGCCCAGCAACG ATACTGGGGAATGGACACCCAGAATATTGCATACGCGCTTGTCCCTGTGTTCTTTATCA CAACAGAAGCAGCAAGATATCGAAGAG-AAAAGGTTGAAAAGATAGAATGACTGAATGAC GCGAATGCTGATGTYTTAAAGGCGATGGTAGCAGATAACAGCCTGTATGATCGTCTGAAAGC CCCGTGACCCCCAGCACACCAGGGAGCCCGCCAGTGAGTCCTGGGCCTTTGTCACCAGGG CCCGTGACCCCCAGCACACCAGGGAGCCCGCCAGTGAGTCCTGGG-CTTTGTCACCAGGG GGGACGCCAGGGAAGCACGTCTGTGGCCATCATCTGCATACGGTGGGCGGTGTTGTCGAG **AGGGATGTGTGTCATCGGTGTAGGCACAAGCGGTGGCACTTTATAAAGCCCACTAACAAG** AGTGGGGCTGAAACCGTCAATGGGGAGGTGCCGGCAACACCTGTGAAGAGAGAACGCAGT GGCACAGAGTAGCAGGTGAGCCGTGGTTTTGGTGACATTGGGGGCAGAGTGGTGGTGCAGGGT GAGGAGAAGGTACTTGGAGCCTCCCAGGTGCTGTGGCAGCATAGGAATGGTATTTGACAG | TCTGCCTAGAGCTTCTTGTAAAGAAGTCACAACTTAGTGCCTCCAGGGGCTTGGCCTTGT TCTGCCTAGAGCTTCTTGTAAAGAAGTCACAAACTTAGTGCCTCCAGGGGCTTGG-CTGT AGGGATGTGTGTCTGTGTAGGCACAAGCGGTGGCACTTTATAAAAGCCCACTAAAAG AGAGTNACAAAAGTGGAGCACAAGTCAAACCAGAAGGAACGGAGAAGCCTGATGTCTGTT GCGAATGCTGATGTCTTAAAGGCGATGGTAGCAGATAACAGCCTGTATGATCCTGAAAGC TCCAGAGAGAGCAGGCGCCCAAGGCGAGGTCACGGTCCTTTCTGTTGGCAGATTT rccagagagagagaccacgcccaaggcgaggrcacggrccrrrcrgrrggarrr AGAGTTACAAAAGTGGAGCACAAGGTCAAACCAGAAGGAACGGAGAAGCTTGATGTCTGTT GGCACAGAGTAGCAGGTGAGCCGTGGTTTTTGGTGACATTGGGGGCAGAGTGGTGCAGGGT 1077 1083 ò

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971 AGAGAGGATTGTTCGCTGCATCATCCAGAATGAAGCCAATGCTGAGGCCTTGAAGGAGAT 1030
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     323 TTGCCACCTGCTTAAGAAGAAAAGGCTATCGTTGTACAACAGAAGCAGAGGCAAGATATCGA
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5.6%; Score 72.6; DB 3; Length 1793;
Best Local Similarity 59.0%; Pred. No. 1.7e-10;
Matches 148; Conservative 0; Mismatches 94; Indels 9
                                                                                                                                                                                                                                                                                                                  Length 1793;
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APPLICANT: Tang, Y. Tom
APPLICANT: Goodrich, Ryle
APPLICANT: Liu, Chenghua
APPLICANT: Ren, Peiyan
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
TITLE OF INVENTION: No. 6919193el Nucleic Acids and
TITLE OF INVENTION: No. 6919193el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802CON
CURRENT APPLICATION NUMBER: US/10/120,988
CURRENT FILING DATE: 2001-01-11
PRIOR APPLICATION NUMBER: 09/774,528
FRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL_Genes Version 2.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                              Score 72.6; DB 3;
Pred. No. 1.7e-10;
0; Mismatches 94;
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Patent No. 6919193
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                      5.6%;
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Best Local Similarity 59.04
Matches 148; Conservative
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                                                                                                           ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (756)..(1667)
US-09-774-528-2
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; LOCATION: (756)..(1667)
US-10-120-988-2
                                     TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
LENGTH: 1793
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                APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

FRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03
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Pred. No. 1.5e-10;
0; Mismatches 94; Indels 9
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APPLICANT: Wang, Dunrui
APPLICANT: Wang, Dunrui
APPLICANT: Dramanc, Radoje T.
TITLE OF INVENTION: No. 674519el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 802
CURRENT APPLICATION NUMBER: US/09/774,528
CURRENT FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 441
SOFTWARE: PL-Lenes Version 2.0
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Zhou, Ping
Goodrich, Ryle
Liu, Chenghua
Asundi, Vinod
Ren, Feiyan
Zhang, Jie
Zhao, Qing A.
Yang, Yonghong
Xue, Aldong J.
Wehrman, Tom
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Best Local Similarity 59.0
Matches 148; Conservative
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ORGANISM: Human
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SEQ ID NO 2
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APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASLESC for Windows Version 4.0
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: A. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10563 ATATATGCTCTTCCTGCTTGTGCTGGTCTTCTTCCTCATGGGCCTGGTAGGCTTCATGAT 10622
                                                                                                                                                          951 CAGGGTGAGGAGAAGGTACTTGGAGCCTCCCAGGTGCTGTGGCAGCATAGGAATGGTATT 1010
                                                                                                                                                                                                                                                1011 TGACAGGGAAGTGGGAGAGCTTTCCTTGACCCCAGGAAGACTGAGGGGGACTGAACATGAT 1070
                                                                                                                                 891 CGCAGTGGCACAGAGTAGCAGGTGAGCCGTGGTTTTTGGTGACATTGGGGGCAGAGTGGTG
                                             831 TCTGTTAGTGGGGCTGAAACCGTCAATGGGGAGGTGCCGGCAACACCTGTGAAGAGAGAA
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Pred. No. 0.00087;
0; Mismatches 26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 16857, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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Best Local Similarity 72.0%;
Matches 67; Conservative
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US-09-949-016-16857
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                                                          920 cdardcccadcrircagcccccrdaggacgargacarg------argaggacacadr 970
                                                                                                          443 TGGGCAAATCGTCCACTACATCATGAAAATGAAGCGAATGCTGATGTCTTAAAGGCGAT 502
                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: GALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
ADDRESSEE: FOLSY & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEPHONE: (703)683-4100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                    RESULT 6
US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 49.6%;
Matches 114; Conservative
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                                                                                                                                                                                                                                                                                                                                     3.53
Best Local Similarity 55.63
Matches 75; Conservative
                                                                                                                                                                                                                                                                         ; ORGANISM: Homo sapiens
US-09-621-976-10505
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                                                                                                                                                                                                                                                                                                                                 263 ATATATTGCATACGCGCTTGTCCTGTGTTTTATCATGGGTCTCTTTGGCGTCCTCAT 322
                                                                                                                                                                                                                                                                                                                                                                      532 ATATATGCTCTTCCTGCTTGTGCTGGTCTTCTTCCTCATGGGCTGGTAGGCTTCATGAT 473
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: TUBERCULOSIS
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                 Gape
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Pred. No. 0.00098;
0; Mismatches 26; Indels 0;
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Pred. No. 1.5;
0; Mismatches 85; Indels 0;
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR PLLING DATE: 2000-10-03
NUMBER: 0F SEQ ID NOS: 207012
SEQ ID NO 16044
LENGTH: 19927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
LENGTH: 4411529
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US-09-621-976-10505
; Sequence 10505, Application US/09621976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
... ORGANISM: Mycobacterium tuberculosis
; OTGANISM: Mycobacterium tuberculosis
; OTGANISM: UFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 1, Application US/09103840A; Patent No. 6294328; GENERAL INFORMATION:
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Best Local Similarity 72.0%;
Matches 67; Conservative (
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Best Local Similarity 53.0%;
Matches 96; Conservative
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US-09-949-016-16044
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US-09-103-840A-1
                                                                                                                                                                              TYPE: DNA
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226 CGAAGAGGCTGTGCGAGCCCTDCCCGGSCCTCCCCAGGGCCCCCCCCCCCCCCTCCTCCTGCC 285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78 CGAAGCGACGCGATGGCTCCGCGGGCACTCCCGGGGTCCGCCGTCCTAGCCGCTGCT 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REPRENCE: 38-10(15849)B
CURRENT APPLICANTON NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2001-07-10
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 8667
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Pred. No. 0.011;
5; Mismatches 55; Indels
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Pred. No. 0.015;
0; Mismatches 116; Indels
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Johert, S.
APPLICANT: Johert, S.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2.
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 10505
LENGTH: 433
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                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10(15849)B
CURRENT PAPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR PILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 918
LENGTH: 9191
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APPLICANT: Pan, Micholas F.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C23
CURRENT APPLICATION NUMBER: US/10/012,231A
CURRENT FILING DATE: 2002-06-10
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 477
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Pred. No. 0.069;
0; Mismatches 116; Indels 0
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                                                                                                                                                                                                                                           Sequence 918, Application US/09902540 Patent No. 6833447 GENERAL INFORMATION:
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Grimaldi, Christopher J.
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
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3.4%;
Best Local Similarity 49.6%;
Matches 114; Conservative (
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Hillan, Kenneth J.
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US-09-902-540-918
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan 1.
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/10/015,389A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper or Palm
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Best Local Similarity 53.2%; Pred. No. 0.12;
Matches 91; Conservative 0; Mismatches 80; Indels
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Fong, Sherman
Gao, Wei-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J
Gurney, Austin L.
Hillan, Kenneth J.
Pan, James
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NAME/KEY: unsure
LOCATION: 3635
OTHER INFORMATION: unknown base
US-10-012-231A-259
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; OTHER INFORMATION: unknown base
US-10-015-389A-259
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Best Local Similarity 53.24
Matches 91; Conservative
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Eaton, Dan 1.
SEQ ID NO 259
LENGTH: 4563
TYPE: DNA
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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APPLICANT: Pan, James
APPLICANT: Pan, James
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830PL10
CURRENT APPLICATION NUMBER: US/10/006,768A
CURRENT FILING DATE: 2002-03-05
NUMBER OF SEQ ID NOS: 477
SPIOT Application removed - See File Wrapper or Palm
SEQ ID NO 259
LENGTH: 4563
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                                              122 CGTCCTAGCCGCTGCTGCTTGGAGGCGCCGTGAGTTCGCCGCTGGT 172
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Job time : 274 secs
                                                                                                                                                                                          Sequence 259, Application US/10006768A Patent No. 6936697 GENERAL INFORMATION:
APPLICANT: Baker: Kevin P.
APPLICANT: Betstein, David APPLICANT: Betstein, David APPLICANT: Eaton, Dan 1.
APPLICANT: Ferrara, Napoleone APPLICANT: Ferrara, Napoleone APPLICANT: Forg, Sherman APPLICANT: Gao, Wei-Qiang
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Fong, Sherman
Gao, Wel-Qiang
Goddard, Audrey
Godowski, Paul J.
Grimaldi, Christopher J.
Hillan, Kenneth J.
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NAME/KEY: unsure
LOCATION: 3635
OTHER INFORMATION: unknown base
US-10-006-768A-259
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ORGANISM: Homo sapiens
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US-10-006-768A-259
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